

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
 An Unit _____ Phone Number 30 _____ Serial Number _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic and describe as specifically as possible the subject matter to be searched. Include the electron species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

Searcher P. Scherzberg
 Searcher Phone # 305-4292
 Searcher Location RM 6A63
 Date 10/14
 Searcher Priority Review Time 13
 Searcher Priority Time 33

Type of Search

NA Sequence # 11
 AA Sequence # _____
 Structure # _____
 Biographic _____
 Citation _____
 Full text _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Quick Pub _____
 JSTOR _____
 Sequence Systems Cambridge
 MATA Internet _____
 Other _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 15:55:36 ; Search time 1779 Seconds
(without alignments)
4.094 Million cell updates/sec

Title: us-09-856-679-31
Perfect score: 2434
Sequence: 1 caagatccgagtggtatat.....cacaccagagaaaaa 2434

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 0.0

Searched: 10 seqs, 1496173 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : *txt:*

- 1: /home/sdavid/sdavid-tmp/oct03/ramirez679/oct9/3108007.txt:*
- 2: /home/sdavid/sdavid-tmp/oct03/ramirez679/oct9/3282154.txt:*
- 3: /home/sdavid/sdavid-tmp/oct03/ramirez679/oct9/3004524.txt:*
- 4: /home/sdavid/sdavid-tmp/oct03/ramirez679/oct9/3023023.txt:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2312.4	95.0	128473	2 AC004241	ACCESSION:AC004241
2	2312.4	95.0	156525	6 AC004241	ACCESSION:AC004241
3	2312.4	95.0	157404	4 AC004241	ACCESSION:AC004241
4	2312.4	95.0	157699	9 AC004241	ACCESSION:AC004241
5	2312.4	95.0	158111	3 AC004241	ACCESSION:AC004241
6	2312.4	95.0	158766	10 AC004241	ACCESSION:AC004241
7	2312.4	95.0	158784	1 AC004241	ACCESSION:AC004241
8	2299.8	94.5	155147	5 AC004241	ACCESSION:AC004241
9	1077.81	44.3	148875	8 AC004241	ACCESSION:AC004241
C 10	577.397	23.7	116389	7 AC004241	ACCESSION:AC004241

ALIGNMENTS

RESULT 1
AC004241
LOCUS
DEFINITION Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.
ACCESSION AC004241
VERSION AC004241
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 128473)
AUTHORS Muzny,D., Aronson,A.D., Adams,C., Bunac,C., Carvelli,K., Cheng,J., Chacko,J., Chen,J., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M., Gorrell,J.H., Haywood,M., Hernandez,J., Jackson,L., Jin,S., Kampal,R., Karpachy,S., Kovar,C., Lau,S., Leal,B., Lee,E., Li,Y., Lichtarge,O., Liu,W., Logan,O., Lu,J., Ly,T., Marondei,I., Martinez,C., Merscher,S., Montgomery,K., Oswal,G., Perez,L., Rashid,N.D., Renault,B., Rowland,K., Savage,L., Scherer,S.E., Shen,H., Simon,M., Stovall,K., Timms,K.M., Todd,J., Vo,O., Williamson,A., Worley,K.C., Yu,W., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 128473)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 128473)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Jul 1, 1998 this sequence version replaced gl:3108007. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
The repeat regions shown were identified using RepeatMasker by Adrian Smit.
Sequence similarities were identified using Powerblast by Jinghui Zhang.
Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.
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Best Local Similarity 16.2%; Pred. No. 5.5e-126;
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Qy 61 GGGGTTTTTGGAGACCAGGGTTTGGAGAGAGTTTCAGCACTGCTGGTAGTTTGGGAATCA 120
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Db 15931 AATGTAGGGAAGAGCAATGGATTGAGGTCCGAACTCGGAGGATCTGCTATACGAGAGCT 15990
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[illegible]

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QY	1711	-----	1710	Db	21871	GGAGGGCAGAGCAGGGGCTCTATGGGTGAGGTAGGCCCAAGGAGCGCTTATGCC	21930
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QY	1711	-----	1710	Db	21931	TTCACCTTTCTGGCTACAGAGGGCAGAGTTTGGGGACCTATGAACAACCCATCT	21990
Db	20851	GCATGGGGCAGGAGATCCTGTGTGAAGACTGGGCTGGAGCATGTGGTGTCCAGTCTCG	20910	QY	1798	-----AGACATGACCTTCATTTCATGAGGAAACACACACTAGTGGAGAATCTCATCAA	1851
QY	1711	-----	1710	Db	21991	CTTTCCACATGACCTTCATTTCATGAGGAAACACACACTAGTGGAGAATCTCATCAA	22050
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QY	1711	-----	1710	Db	22051	CTTTGAGAAGATGGTGTAGTCCAGGAGAGAGAGCACTTCACTACTAACATAGTTGGAGGA	22110
Db	20971	CCTGTGTCAACAGGGCTGTCTGCCCTCAGGAACCTCCAGAGGCTTCCGGGCTAGACC	21030	QY	1864	-----	1863
QY	1711	-----	1710	Db	22111	CATGACTGTGCTGGGAAGGGGAGGCTTGGAGGCAGCTTAAACATTGTTATGAATAT	22170
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QY	1711	-----	1710	Db	22171	ATGAGATGAATACTTACTGTGTATAGCCCCCTGCTTATCCACTGCAACTGGGTCTGC	22230
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Db	21211	CTGCAGAGAGAGAGGAGGACACAGAAAGAGACAGGGATAGAAAGGACAGAGAGGT	21270	QY	1864	-----	1863
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QY	1711	-----	1710	Db	22411	CTTGGTTCAGAGGAGCTTGGCTGCCCTGCTGTGCACAGGCGAGGACAGAGGTTTCTCCC	22470
Db	21331	TCAGTGCTAATGGGAGTTGGAAGCCCGTGTTCGCCCTGTGACAGAGCCTGGGTGAGACC	21390	QY	1864	-----GAGAATGATGCCAGAGCCGCGCGGA	1889
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QY	1711	-----	1710	Db	22531	TGCTGCACCACTGCGGAAGCCACACACCTGCTGTGAGAGGGCGGTCCCGGGGTGGGAGGT	22590
Db	21451	CCTCCTTGGTGGGTGTGTGGTGTATGGTGTGTGCAACCCCTCAGTGTGGC	21510	QY	1919	-----	1918
QY	1711	-----GGATCCCTCATGGAACCAACCGGGTATACCGACTGGCCCTGCCAAGCTC	1759				

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Q	y	1919	-----GNGCCTCTCTCACTCAGAAAGCCGAGTTTCCCACTCCACGAGACAGCC	1970	D	b	23731	AACATAGTAGTATGTTCCAGGCCAGCCAGAGTGGCGTGGCAGGGAGGCTGAGGCCCG	23790
D	b	22651	CCCCGAGTGGCTCTCTCACTCAGAAAGCCGAGTTTCCCACTCCACGAGACAGCC	22710	Q	y	2424	-----	2423
Q	y	1971	AGTGGCGAGGATTTCACAT-----	1991	D	b	23791	CCCTCTGGGAAGGAGCTGTGGAGGAGAAGCAGCCCCATGCTGGCACGGCCAGACTGGG	23850
D	b	22711	AGTGGCGAGGATTTCACATGTAAGTGGTGGCGATGGTGGTGGCGAGGGGGTG	22770	Q	y	2424	-----	2423
Q	y	1992	-----	1991	D	b	23851	TCCAAGATCTGATGCCACCCAGATGTCTCCAGGGCTCTGGCAAAGGGCGGCTGGA	23910
D	b	22771	CTTATGTAGTTACCCATGCTGGCACATCTTAGGCATTTGCCATGTGCCAGCAGGAG	22830	Q	y	2424	-----	2423
Q	y	1992	-----	1991	D	b	23911	GCCTGGAGCCCTGTGACGAGCAGCCAGGGTGACCATCAGCTCCCGCTGGTGGTCCAAT	23970
D	b	22831	CCCGGCCCTTCCATACATGATGTTGATAATGTTTCAGCCTCTGTGCTTGAGCCAGGGGC	22890	Q	y	2424	-----	2423
Q	y	1992	-----	1991	D	b	23971	AGGACTTTACAGTCCAGATGCAACTGACAGCTTTCTTCCCAACTGCAATCCCCGCTTTTCC	24030
D	b	22891	TCCTCGCTCCCTCACCCGTGGGTGGGCAGGCAGCCGCTCTTAGGAATTGGTGATGG	22950	Q	y	2424	-----	2423
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D	b	22951	GAAGTGGTGGTGGGTGGAGGGCAAGAAGCAGATGTATGGCTCTCTTGAGGGG	23010	Q	y	2424	-----	2423
Q	y	1992	-----GCT	1994	D	b	24091	TGATAGAAACAATGCTGAAGCTTCCCGGGAGAGCCCGTTCGCTTGTGAGGCCCAACAGAC	24150
D	b	23011	AAAGTTGGTTCCCAAAAGGGGCATCAGTGCTCCTGACTACTCTCTCCACACAGGCT	23070	Q	y	2424	-----	2423
Q	y	1995	CGAGCAGTCCCTGAGCACCCGAGTCCAGCCAGCACCCTGGGCTTATGTCCAGCAGTGA	2054	D	b	24151	TTCCAGGAATCAGGGTTTATCATCAGTGTGAGATGGTCCCGCAAGCTCTGGTCATA	24210
D	b	23071	CGAGCAGTCCCTGAGCACCCGAGTCCAGCCAGCACCCTGGGCTTATGTCCAGCAGTGA	23130	Q	y	2424	-----	2423
Q	y	2055	AGCTATTGACACACCGCGGAATCTCCGCCCTCTCCGAGAGCTGGAGCCATGAGGAG	2114	D	b	24211	CGAAGTCTCTCTTCCCTGCCCCCTTCAGCACTTCCCCCTAGGAACAGCTACTCCAGGAC	24270
D	b	23131	AGTCTATTGACACACCGCGGAATCTCCGCCCTCTCCGAGAGCTGGAGCCATGAGGAG	23190	Q	y	2424	-----	2423
Q	y	2115	GGCTGGGACTGGAGTGGAGCAGGCACTTGACGCCGGGAAAGCCAGGGTGTCCGGGCC	2174	D	b	24271	GCCTTTGCGAGCAGAGCTCACCCAGGAAGCTCCAGGGACTCCACCCCTTTGCCCTTGCT	24330
D	b	23191	GGCTGGGACTGGAGTGGAGCAGCACTTGACGCCGGGAAAGCCAGGGTGTCCGGGCC	23250	Q	y	2424	-----	2423
Q	y	2175	AGATACTCACAGGCTGGCCACAGCTGGGCAAGGCTCTCGTGGATGGACTCGAGTCCC	2234	D	b	24331	ATTGCCCTGAGTCTTGGCAGCAGGAGGCACTTGTCTGGCCAGAGAGAGAATCATGGCCC	24390
D	b	23251	AAGATACTCACAGGCTGGCCACAGCTGGGCAAGGCTCTCGTGGAGTGGACTCGAGTCCC	23310	Q	y	2424	-----	2423
Q	y	2235	TGAGCAGGCAGTGTGGAGCAGCCATCCCTGTGATGACTGGCAGCTAAGGAGGACCTC	2294	D	b	24391	CTGGCATGACTCTGTAGTAGGTATTGAGGCTGCAGGGCCCTTGGCGTCCAGAGGACGCTG	24450
D	b	23311	TGAGCAGGCAGTGTGGAGCAGCCATCCCTGTGATGACTGGCAGCTAAGGAGGACCTC	23370	Q	y	2424	-----	2423
Q	y	2295	GGAGTGGACCCGACCGAGGAATAACGAATGACCCAAAGGCCAAGGAAGGAGGACAGAGAG	2354	D	b	24451	GTATGCCCTCTGCACCTTCAGCCCCATGGATGGGATACACAGGCTGCTGTCTCCAGA	24510
D	b	23371	GGAGTGGACCCGACCGAGGAATAACGAATGACCCAAAGGCCAAGGAAGGAGGACAGAGAG	23430	Q	y	2424	-----	2423
Q	y	2355	GCCCCAGAGTGGGTGGAGTGGATGGCTGGGACGTTGTGTGCAATAGAGAGTCTC	2414	D	b	24511	AAGGGTCAGAGCCCTTTAGCAGGGAGGCACACAGCTGGGCTTAGACCTCAGGTCACATAAG	24570
D	b	23431	GCCCCAGAGTGGGTGGAGTGGATGGCTGGGACGTTGTGTGCAATAGAGAGTCTC	23490	Q	y	2424	-----	2423
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D	b	23551	TTATTTTACAGTGGACAGAGAGAGAGAGAGGCTGCATGTGTACCGTGTGTGGCAA	23610	Q	y	2424	-----	2423
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D	b	23611	GGCAGGCGCTTGGCTGGGCGAGGGCCCCCTGCTTTCTTTCCACAGCTTTTCTTCCAAC	23670	Q	y	2424	-----	2423
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QY	2424	-----	2423
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RESULT 2

AC004241

LOCUS

DEFINITION

AC004241

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

156525 bp DNA linear HTG 28-MAR-1998
Homo sapiens, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.
AC004241
GI:2995474
HTG: HTGS_PHASE1.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 156525)
Muzny,D., Aronson,A.D., Brundage,E., Carvelli,K., Chen,E., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesha,R., Garcia,C., Goodman,M., Correll,J.H., Haywood,M., Jackson,L., Kampal,R., Karpthy,S., Leal,B., Li,Y., Liu,W., Logan,O., Lu,J., Ly,T., Martinez,C., Osawai,G., Perez,L., Rashid,N.D., Rowland,K., Savage,L., Scherer,S., Shen,H., Timms,K.M., Todd,J., Vo,Q., Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 156525)
Worley,K.C.
Direct Submission
Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[WARNING] On Apr 1, 1998 this sequence was replaced by a newer version gi:3004524.
On Mar 28, 1998 this sequence version replaced gi:2980958.
* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* *	*	1	52081: contig of 52081 bp in length 52082 52101: gap of unknown length 52102 52174: contig of 40273 bp in length 92375 92394: gap of unknown length 92395 132274: contig of 39880 bp in length 132275 132294: gap of unknown length 132295 151994: contig of 19700 bp in length 151995 152014: gap of unknown length 152015 153710: contig of 1696 bp in length 153711 153730: gap of unknown length 153731 154435: contig of 705 bp in length 154436 154455: gap of unknown length 154456 155157: contig of 702 bp in length 155158 155177: gap of unknown length 155178 155862: contig of 685 bp in length 155863 155882: gap of unknown length 155883 156525: contig of 643 bp in length.
FEATURES			
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BASE COUNT	45450 a 35421 c 34266 g 41224 t	164 others	
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Query Match	95.0%; Score 2312.4; DB 6;	Length 156525;	
Best Local Similarity	16.2%; Pred. No. 4.5e-126;		
Matches 2433;	Conservative 0;	Mismatches 1;	Indels 12584; Gaps 12;
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Qy	121	CCCATGTGCCAGGCGACACATGAGCGCAGTAGTAAGAACTCTTCGAGGGGTCCCTGAGATTGGA 180	
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Db	54049	GTGATACATAAGTATTAGCTGCTATTATTATCATCATTTGTGTTAGTCAATTAATATGA	54108
Qy	1163	-----	1162
Db	54109	ATTAATAACAATCTCATGAGATACAGGTACTTTATTCCTATTTTCAGACAAGAACTGA	54168
Qy	1163	-----	1162
Db	54169	AGCTCAAGGGCATGAGCTATTCCCTCAAGCTCACACAGTAGAGTAGCTGGTCTTGGAAAC	54228
Qy	1163	-----	1162
Db	54229	TTAAGTAGTCTTCATTTGTTTAGTCACCTCAGCAACATTTTGTGAGGATCAGCTATGAGCC	54288
Qy	1163	-----	1162
Db	54289	AGCAATATGTTAGGAGCTGGAGATACCACAGCAGGTAAACAGGTACAGCTTGATGTTAA	54348
Qy	1163	-----	1162
Db	54349	GAGCATAGCGTGGACTCCACAGCCGTGAAGGCATCTTAGGCTCACCATTTACTAGCT	54408
Qy	1163	-----	1162
Db	54409	GTGTGATGTGGCAAGTTGCTTAACCTCTCTGAGCCTGCAATTCCTCACCTGCAGATG	54468
Qy	1163	-----	1162
Db	54469	AGGACTGTAATTGTATCTACCCACAGGGTTGCAATGGCTAAAGTAGAGCTAAATGTGTAAA	54528
Qy	1163	-----	1162
Db	54529	GCATTAGCACAGGGCTGCCAGTCAGTCGTGAGAACATGGCGGGCTCAGGAGATTAAAG	54588
Qy	1163	-----	1162
Db	54589	ATGGGCTCCAGAGAACCTGGAACATTTCAAAACCACCTGTTCTCTCGGAGGGCACGGCT	54648
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Db	54649	TGACAGCTGGAACCCAGGGCAGACAAGAAATTAGGGGGGTTCAAGAAAGTGGGGATGAGAAA	54708
Qy	1163	-----	1162
Db	54709	AGAAAGCCTTCTCCCTTCAGGAAGTGGGGAGAGATGGTCACCTGTGTGCCCTGCCCTGG	54768
Qy	1163	-----	1162
Db	54769	GAAGCACTGCCCTCTGCTGGCCACCTGGTGAGTTGCAGTTGCCAAAGGTCATGTTATT	54828
Qy	1163	-----	1162
Db	54829	GAGACCCTACTATGTGCCAGGCACCTGTTTAGAGCACTGATCTCCGAAGCACTTGGATCGA	54888
Qy	1163	-----	1162
Db	54889	CACCCATGTCATAACCAACATTTAATTAACCCACACCCCACTGTGTGAATATTGTTT	54948
Qy	1163	-----	1162
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Qy	1163	-----	1162
Db	55009	TTGATGGAGTAGAAATGCAAGCAGGTAGAAAAAGTAAACGTAAGTAGAAGAGCTCATAT	55068
Qy	1163	-----	1162
Db	55069	TTTCCCAGGCACATGGATGATGTACCTTACTTACTTGGAGGCCACTGCTCTAGGGAC	55128
Qy	1163	-----	1162
Db	55129	TGGGACTCAAGCACACAGTCCAGTCCATGAGGAGCTGATGAAAAATCAACACCAAGGCTTA	55188
Qy	1163	-----	1162
Db	55189	TATAAGACACTTCCCAATTTTCAAGGGCTTTTATACATAGCATGTACTTATAGTACTA	55248
Qy	1163	-----	1162
Db	55249	TTTATATACATTTATTTATTTGACTTATGAATAGTTGGGCAAGTCTTATTGTCTCCAT	55308
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Db	55309	TTTACCAGGGAAGAAAGTGAAGCTGAGGAGGCTCAGACCCCTGCCAGGTTCCTCTGAC	55368
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Db	55369	TCACTGAGAACTTTTCTCATCTCTTGGATGTCTTCCCTGGGCTGCGTGGCTGGTGG	55428
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Db	55429	GCATGCACTGTGTTATCTGAGCACCCAGGACTTCAACCCCGCTACTAGGAGAAA	55488
Qy	1163	-----	1162
Db	55489	CAACCTCTCAGCCTCCCAACAGCACCTCCACCTGGCATCCAGCTGGTCCCCGGCCTCC	55548
Qy	1163	-----GATGCCATTGGCCTGCAGCCA 1183	
Db	55549	CTCCCTTCCCCACCACAGTCCGCCCTGCTGCTTTTGCAGATGGCATTGGCCTGCAGCCA	55608
Qy	1184	GATGCCCTGTGTGGCCACATCTCTGGGGCTCAATGAGCGTCTCTTTGTTGTCACACCCA	1243
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Qy	1244	CAGGAAGTGCATGAGCT----- 1260	
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Qy	1261	-----	1260
Db	55729	TTTTGAGTGTGGCAGTGGTGGATTCTGGGGAGGGTCCCAGGAGAGAGAGAGGGGCG	55788
Qy	1261	-----	1260
Db	55789	CTGGCTCTGGCTGCTGGGTCTCAGCACACAAAGAGTGGGCTCAGCTGATGGGG	55848
Qy	1261	-----	1260
Db	55849	AATTTCCAAGATAGTGCAGGGCAGGGGCTGGTAGCACTGGTTGGAGCTCCCAAGAGAA	55908
Qy	1261	-----	1260
Db	55909	AGAGGAGGACCTGCCCTAGTTAGGGGTTCCCCAGGAGACAGGAGCCCCAAAGAGGGGTC	55968
Qy	1261	-----	1260
Db	55969	TCAGCACTGGGAGGCCCTATCTCCAGCTGCTATAGCCCTTAGACACCCCTTACTCTCCA	56028
Qy	1261	-----	1260
Db	56029	CTCTGCCCTCTTAACCCCTCTCTTAACACGAGCATAGAGTCTTTGCCCCAACCCCTCTCC	56088
Qy	1261	-----	1260
Db	56089	CCCTACCTGTGCCCTTTCCCTTGGATTCTCAGGCAGGCCCTGAGCACTCTCTCCACCCGC	56148

Db	58309	GGAGGGGCGAGAGGAGGGGCTCTATGGGGTGAGGTAGGCCCAAGGAGCGCTTATGCC	58368
Qy	1798	-----	1797
Db	58369	TTCACTTTTCTGGGCTACAGAGGGCAGAGTTTGGGACCTATGAACAAACCCATCT	58428
Qy	1798	-----AGACATGACCTTCATTATGAGGGAACACACACTAGTGGAGAATCTCATCAA	1851
Db	58429	CTTTCGACAGATGACCTTCATTATGAGGGAACACACACTAGTGGAGAATCTCATCAA	58488
Qy	1852	CTTTGAGAGAT-----	1863
Db	58489	TTTTGAGAAGATGGTGTAGTCCAGGAGAGCAGGCATTCACTACTAATAGTTGGAGGA	58548
Qy	1864	-----	1863
Db	58549	CATGACTGTGGCTGGGAAGGGCAGGGCTTGGAGGCAGCTTAAACTTGTATGAATAAT	58608
Qy	1864	-----	1863
Db	58609	ATGAGGATGAATACTTACTGTGTAAATAGCCCTGCCTTATTCCTACTGCAACTGGCTGC	58668
Qy	1864	-----	1863
Db	58669	CAGGCTGCCAGCCTCAGACGTCTACCATTTCAACGAGAGCCCTTCCAGCCCTCTTCTCTC	58728
Qy	1864	-----	1863
Db	58729	TAAGCCTTCTCTCTGGCTCTGCCTTCTGTCTCTGCTGCTGCCGCTGGGCTCTG	58788
Qy	1864	-----	1863
Db	58789	GGTGTGCTGAGCGAAGTACACATGATGCCACATAACCAAGGATCTTACAGTCCCTGATC	58848
Qy	1864	-----	1863
Db	58849	CTTGTTCAGAGGAGCTTGGCTCCCTGCTGCTGCACAGGCGCAGACAGGTTTCTGCC	58908
Qy	1864	-----CAGAAATGATGGCAGAGCGCGCGGA	1889
Db	58909	TCAGCAAGAGGTTATGCCCGGTTGTCCGACAGAAATGATGGCAGAGCGCGCGGA	58968
Qy	1890	TGCTGCACCACTGCCAAGCCACAACCCCT-----	1918
Db	58969	TGCTGCACCACTGCCAAGCCACAACCCCTGGTGAGAGGCGGGTCCCGGGTGGAGGT	59028
Qy	1919	-----	1918
Db	59029	CCCCACCCCTACATCCTCTGTGAGGCTCCAGGGTGGCCCTGACTCCATGACCCCTCCCCA	59088
Qy	1919	-----GTGCTCTCTCACCACTCAGAAAGCGAGTTCCACCTCCACAGGACAGCC	1970
Db	59089	CCCCCGCAGTGGCTCTCTCACCACTCAGAAAGCCGAGTTTCCACCTCCACAGGACAGCC	59148
Qy	1971	AGGTGGCGAGGATTTCCACAT-----	1991
Db	59149	AGGTGGCGAGGATTTCCACATGTAAGTGGTGGCGCATGGTGGTGCGCAGGAGGGGTG	59208
Qy	1992	-----	1991
Db	59209	CTTATGGTAGTTACCCATGGCTGGCACATCCTTAGGCATTTGCCATGTGCCAGGCGGAG	59268
Qy	1992	-----	1991
Db	59269	CCCGGCCCTTCCATACATGATTTGATAATGTTACGCTCTGTGCTGAGCCAGGGGGC	59328
Qy	1992	-----	1991
Db	59329	TCCTCGTCCCTCACCGTGGGTGGCAGGACAGCGCTTTTAGGAAATTGGTGATGG	59388
Qy	1992	-----	1991
Db	59389	GAAGTGGTTGGTGGTGGAGGCGAAGAGGCGAGATGTATATGGCTCTTGGAGGGG	59448
Qy	1992	-----GCT	1994
Db	59449	AAAGTTGGGTTCCAAAGGGGATCAGTGCCTCCCTGACTACTCTCTCCACACAGCT	59508
Qy	1995	CGGACACTCCTTGAGCACCCGGAGTCCAGCCAGCAGCCTGGGCTTATGTCCAGCAGCTGA	2054
Db	59509	CGGACACTCCTTGAGCACCCGGAGTCCAGCCAGCAGCCTGGGCTTATGTCCAGCAGCTGA	59568
Qy	2055	AGGTCAATTGACAAACAGCGGGAACCTCTCCCGCTCTCCGAGAGCTGGAGCCATGAGG	2114
Db	59569	AGGTCAATTGACAAACAGCGGGAACCTCTCCCGCTCTCCGAGAGCTGGAGCCATGAGG	59628
Qy	2115	GGCTGGGACTTGGAGCTGGAGCAGCACTTGAGCCGGGAAAGCCAGGCTGTGCCGGGCC	2174
Db	59629	GGCTGGGACTTGGAGCTGGAGCAGCACTTGAGCCGGGAAAGCCAGGCTGTGCCGGGCC	59688
Qy	2175	AAGATACACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGPGAGTGGACTTCGAGTCCC	2234
Db	59689	AAGATACACAGGCTGGGCAAGGCTCTCCGPGAGTGGACTTCGAGTCCC	59748
Qy	2235	TGGACAGGCACTTGGAGGAGCCATCCCCTGTGATGACTGGCAGCTAAGGAGGACCTC	2294
Db	59749	TGGAGCAGGCACTTGGAGGAGCCATCCCCTGTGATGACTGGCAGCTAAGGAGGACCTC	59808
Qy	2295	GGAGTGGACCCGAGCAGGAATAACGAATGACCCAAAGGCAAGGAGGAGCAGAGAG	2354
Db	59809	GGAGTGGACCCGAGCAGGAATAACGAATGACCCAAAGGCAAGGAGGAGCAGAGAG	59868
Qy	2355	CCCCAGGAGTGGTGAGAGTGGGCTGGGACGTTGTGTCGAATAGAGAGTCTC	2414
Db	59869	CCCCAGGAGTGGTGAGAGTGGGCTGGGACGTTGTGTCGAATAGAGAGTCTC	59928
Qy	2415	CACACCAGA-----	2423
Db	59929	CACACCAGATGCTTCCAGATTTCTGCTGCTCTGGCTTTGTGTCCAGCCAGGCTGCAGT	59988
Qy	2424	-----	2423
Db	59989	TTATTTTTCACAGTGCACAGAGAGAGAGAGAGGCTGCATGTGTACCGTGTGTGGCNA	60048
Qy	2424	-----	2423
Db	60049	GGCAGGCGCTTGGCTTGGGCGAGGGGCCCTGCTTCTTCTTCCACAGCTTCTTCCAAAC	60108
Qy	2424	-----	2423
Db	60109	AGCAGGCGAGTGGGGCTGGCGGCTGTGCGGTGGTCCCTGAGGAGCTTTATTTGTACTGTC	60168
Qy	2424	-----	2423
Db	60169	AACATAGTAGTATGTTCAGGCCACCCAGAGTGGGCGTGGCAGGAGGCTGAGGCCCG	60228
Qy	2424	-----	2423
Db	60229	CCCTCTGGGAAGGAGCTGTGGAGAGAGAAGCAGCCCATGCTGGGCACGGCCAGACTGGG	60288
Qy	2424	-----	2423
Db	60289	TCCAAGATCCTGATGCCACCCAGATGTGCTCCAGGGCTCTGGCCAAAGGGCGGCTGA	60348
Qy	2424	-----	2423
Db	60349	GCCTGGAGCCCTGTTCAGCAGCCAGGCTGACCATCAGTCCCCCTGGTGGTGGTCCCAT	60408
Qy	2424	-----	2423
Db	60409	AGGACTTTACATCCAGATGCAACTGACAGCTTCTTCCCACTGCAATCCCCCGCTTTTCC	60468
Qy	2424	-----	2423
Db	60469	ACACTTGAGCTCGCTGGCGTGTGGCCAGGCTTCTGGGCTTCTTCTGGGGTGGCTTG	60528

Qy	2424	-----	2423
Db	60529	TGATAGAAACAATGCTGAAGCTTCCGGGAGAGCCCGTCGCTTGTGAGGCCCAACAGAC	60588
Qy	2424	-----	2423
Db	60589	TTCCAGGAATCAGGGTTTATCATCAGTGTGAGAAATGTTCCAGCAAGCTCGGTGATA	60648
Qy	2424	-----	2423
Db	60649	CGAAGTCCTCTCTCCCTGCCCTTCAGCACTTCCCTAGGAACAGCTACTGCCAGGAC	60708
Qy	2424	-----	2423
Db	60709	GCCTCTTGCAGGAGAGCTCACCCAGGAAGCTCCAGGACTCCACCCCTCTTGCTTGCT	60768
Qy	2424	-----	2423
Db	60769	ATTGCCCTGAGTCCTGGCAGCAGGAGGCACTTGTCTGGCCAGAGAGAACTCATGGCCC	60828
Qy	2424	-----	2423
Db	60829	CTGGCATGACTCTGAGTAGGTATTTGAGGCTGCAGGGCCTTGGCGTCCAGAGCGACTG	60888
Qy	2424	-----	2423
Db	60889	GTATGGCCCTCTGCACCTTCAGCCCATGGATGTGGATACACAGCGCTGTGCTTCCAGA	60948
Qy	2424	-----	2423
Db	60949	AAGGGTCAGAGCCTTTAGCAGGAGGAGCAGCAGCTGGGCTTAGACCTCAGGTCACCTAAG	61008
Qy	2424	-----	2423
Db	61009	TGAATCTGACAAAGTCAGTGAACAGTCTCTTCTTCATTTCTCCACCTGTAGCCAGGT	61068
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	61309	CAGGACAGGAGGTCAAGCCTGGGTGAGTCAGGAGTCCGGGGCTTTCTTTTCATCCAAC	61368
Qy	2424	-----	2423
Db	61369	CCATTGCTGCTGCTCGGCAAAAGCCAGCCAGCCGTCGGCCCTTCACCGTTCT	61428
Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	61969	AGAAGAAGTGTGCAGAAAGGGAGTGTGGCCCTAGATCAGTCTCTTTAAAAAGCTCTGTT	62028
Qy	2424	-----	2423
Db	62029	ACCTGAAGGAGGTCAAGCAGAGAGAGGAATGGCTGCGTGTGTGTCTTACCGGGCAGGACAG	62088
Qy	2424	-----	2423
Db	62089	GACAGAGGAGGTCAATTGTTTACACACACATCCCCCTCTCTCTCTCCCTCCACCTT	62148
Qy	2424	-----	2423
Db	62149	CCCTGTGAAGCCTGAGCAGGCTGTGGCCAGGCTCAGGCCCTGACTGTGGGTACACAC	62208
Qy	2424	-----	2423
Db	62209	CAGGAGGGCCACCGCTCCCCACAGACAGGGGTGGAGTGGTCACTGAGGAGCCAGCACCTCT	62268
Qy	2424	-----	2423
Db	62269	GCTGCTCAGCATCTCCGCTGGGCCAGCTGTCCCTCTCTCTCAGGCTCCATCCGAAC	62328
Qy	2424	-----	2423
Db	62329	AAAAGGAAGCAGAGCCTGAGATCCGGCACCCCATCCCTCCACTCAGCACTGAGTTAG	62388
Qy	2424	-----	2423
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Db	62449	CCCTCAGCCTCTGGCTGCTCTCTTCCCAATAGTCACAGATTTACCATGATATAATAG	62508
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Qy	2424	-----	2423
Db	62569	TTTTTATCTGATGACAGAATAGGTACTACAGGTATTTTACTCTCTGTTTTTACAGTCAA	62628
Qy	2424	-----	2423
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Qy	2424	-----	2423

Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	64969	GCCAGTTTCACCCTCTCAGCGTTGCTGGGCTGAGCCCTGCAGGAGCAACCTGTGTGCTG	65028
Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	65089	CTGTTTCTCTCTCCGGTTCTTGACTTTGCACCAGGAGCTGTGGAATATCTCATCAAT	65148
Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	65869	AATCTCCACCTCCTGGTTCACGGATTCCTGCTTAGCCTCCCAAGTAGTGGGATT	65928
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Qy	2424	-----	2423
Db	66049	CAAAGTCTGGGATTACAGGGTAAGCCACCGGCCCCAGCCACAGAACATTTGTTAAACATT	66108
Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	66289	TCTACGGGGAAATTGAGGCACAGAGGGGTGAGGAACTTGCCCGAGGATTGTACAGCTGG	66348
Qy	2424	-----	2423
Db	66349	TGGTGGCAGAGCTGGGATTCAAACCCAGGCAGCTTGGCTTTAGAAATCAACAGTCTGAGC	66408
Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	66709	CAGCCCAAGCTGTGCCAACATACCTGGGGCGAGAGCAGCCCATGTTCTCACGCCAGCGG	66768
Qy	2424	-----	2423
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	66889	ATTGTGCTCTAGACCCCTCTTTAAAGCCAGTGGAGTTTGAGACATGCAATAGTAATTTT	66948
Qy	2424	-----	2423
Db	66949	ATAATCATTTACTGGCAGTGTAAACAACATTTAGCACACTGGCAAGAGTGTAGGCAG	67008
Qy	2424	-----	2423
Db	67009	ATGTTCTCTTGGGATCTTAAAGAGGAGGATACAGTGTGAGATCTCTGTGCACACTGTGA	67068
Qy	2424	-----	2423

Db 67069 TTCAGAAACTGCTGGAACCTGCTCCAGTCCCTGTGTGGTGGCTGCCCTTGTAGGGGTGGTGCC 67128
QY 2424 ----- 2423
Db 67129 AAGGCTGGCTTGGGGTTTAGTCTCTCCTAAATTTCCATTTAGGCCCAACRAATACACAA 67188
QY 2424 -----AAAAA 2434
Db 67189 TATAGCTAAAAA 67206

RESULT 3
AC004241
LOCUS AC004241 157404 bp DNA linear HTG 04-APR-1998
DEFINITION Homo sapiens, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.
ACCESSION AC004241
VERSION AC004241 GI:3023023
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 157404)

Muzny, D., Aronson, A.D., Brundage, E., Carvelli, K., Chen, E., Di, W.,
Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C.,
Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L., Kampal, R.,
Karpatis, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., Ly, T.,
Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Rowland, K.,
Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J., Vo, Q.,
Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
Direct Submission
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
2 (bases 1 to 157404)
Worley, K.C.
Direct Submission
Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[WARNING] On Apr 13, 1998 this sequence was replaced by a newer
version gi:3046263.

On Apr 4, 1998 this sequence version replaced gi:3004524.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 52081: contig of 52081 bp in length
* 52082 52101: gap of unknown length
* 52102 92893: contig of 40792 bp in length
* 92894 92913: gap of unknown length
* 92914 132793: contig of 39880 bp in length
* 132794 132813: gap of unknown length
* 132814 152574: contig of 19761 bp in length
* 152575 152594: gap of unknown length
* 152595 154290: contig of 1696 bp in length
* 154291 155295: contig of unknown length
* 155296 155315: contig of 985 bp in length
* 155316 156019: contig of unknown length
* 156020 156039: contig of 704 bp in length
* 156040 156741: gap of unknown length
* 156742 156761: contig of 702 bp in length
* 156762 157404: contig of unknown length
* 157405 157404: contig of 643 bp in length.

FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 45692 a 35598 c 34547 g 41402 t 165 others
Query Match 95.0%; Score 2312.4; DB 4; Length 157404;

Best Local Similarity 16.2%; Pred. No. 4.5e-126;
Matches 2433; Conservative 0; Mismatches 1; Indels 12584; Gaps 12;
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Db 52707 CAAGGATCCGATGGGTATATGAGGTGAGGTAAATGATCATTTATGTTGGAGGATGCGAG 52766
QY 61 GGGGTTTTGAGACCAGGGTTTGGAGAGAGTTTCAGCACTGCTGCTAGCTTTTGGGAATCA 120
Db 52767 GGGGTTTTGAGACCAGGGTTTGGAGAGAGTTTCAGCACTGCTGCTAGCTTTTGGGAATCA 52826
QY 121 CCATGTGTCAGGCGACACATGAGGCAGTAAAGAACTCTCCAGGGGTCCCTGAGATTTGGA 180
Db 52827 CCATGTGTCAGGCGACACATGAGGCAGTAAAGAACTCTCCAGGGGTCCCTGAGATTTGGA 52886
QY 181 AATGTAGGAAGAGCAATGGATTGAGTCCGAACTGGAGGATCTGCTATACGCGAGCT 240
Db 52887 AATGTAGGAAGAGCAATGGATTGAGTCCGAACTGGAGGATCTGCTATACGCGAGCT 52946
QY 241 GGGAGGAGGACAGAGTACAGTACAGAGTCCGAAAAAGCAGGTTGGGAAGGGAACCTG 300
Db 52947 GGGAGGAGGACAGAGTACAGTACAGAGTCCGAAAAAGCAGGTTGGGAAGGGAACCTG 53006
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QY 781 TGAGCTCAGGTGAATGTGGCAAGCAGAGCCCTCTGGTGTGTAATGCTGTGGCGGCC 840
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Qy	1015	-----	1014
Db	53907	GGGCTCCCACTGCAGCTCAGCCTCTTGGGGATCCCTCCACCAATTAATGCAATAGCC	53966
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Db	54087	TGACAGCTCCGTCGAGAGAGGTGATGCGACGTTGGCCAGGAGGATGGCTGCACCAAGG	54146
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Db	54747	TTAAGTAGTCTTCATTTGTTTGTAGTACTCAGCAAAACATTTTTCAGGATCAGCTATGAGCC	54806
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Db	54867	GAGCATAGAGGTGGACTCCAGACCGTGAAGGCATCTTAGGCTCACCATTACTAGCT	54926
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Db	54927	GTGTGATGCTGGCAAGTTGCTTAACCTCTCTGAGCCTGCATTTCTCACCCTGTAGATG	54986
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Db	55227	AGAAAGCCTTCTCCCTTCAGGAAGTGGGAGAGATGGTCACCTGTGTGCCCTGCCCTGG	55286
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Db	55467	TGTAAGTAATACATATATTACTACATTAATATCATATAATATAAGATAGATAAATAAGAA	55526
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Qy	1163	-----	1162
Db	55827	TTTACCAGGAAGAAAGTGAGGCTGAGGAGGCTCAGACCTCGCCAGGTTCTTCTCTGAC	55886
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Db	55887	TCACTGAGAATCTTTCTCTCATCTTGGATGTGCTTCCCTGGGCTGCGTGGCTGCGTGG	55946

Db	58107	CTGGGAGCTCTTGAGAGAAATCCACCTCGTGGGGCTCAAGGGATTCAAAGGAGTTTACT	58166	QY	1864	-----	1863
QY	1711	-----	1710				
Db	58167	CTCAGAGAGAGAGGGGACACAGAAAGACAGAGGATAGAAAGGACAGAGAGT	58226	Db	59247	TAAGCCCTTCTCCTGGCCCTCGCCTCTGTCTGTGCTGGTCCCGCTGGGCCCTCTG	59306
QY	1711	-----	1710	QY	1864	-----	1863
Db	58227	GACAGTGACAGACTTTTCCAAGAAACCTGGGGCCCTGTGACTAACTGTGTAATTTTC	58286	Db	59307	GGTGTGTGAGGCGAAGTACACATGATGCCACATAACAAGGATCTTACAGTCCCTGATC	59366
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Db	58287	TCAGTGTCTAATGGAGGTTGGAAGCCCGTGTTCGCTGTGACAGAGCCTGGGTGAGACC	58346	Db	59367	CTTGGTTACAGAGGAGCTTGGCCTCCTGCTGTGCACAGGCGAGGACAGGTTTCTCCC	59426
QY	1711	-----	1710	QY	1864	-----	1863
Db	58347	TGGGGCTGAGGAGAGGTGAGTTGGGGCCCTCTGCACCTGCTGTGGGATGGGCATGTGGCC	58406	Db	59427	TCAGGCAAGAGCTTATGCCCGCGTGTTCGCGCAGAGAATGATGGCCAGAGCGCGCGGA	59486
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QY	1711	-----	1710	QY	1919	-----	1918
Db	58467	TTCTTCCCTTAGGATCCCTCATGGAACCCACCGGTATACCGACTGGCCCTCGCCAAAGCTC	58526	Db	59547	CCCCACCTTACATCCTCTGTGAGGCTCCAGGGTGGCCCTGACTCCATGACCCCTCCCCA	59606
QY	1760	TCCCTCTCTGTCATCCCTTCATGCCCCCTTCTTCTCAA	1797	QY	1919	-----	1918
Db	58527	TCCCTCTCTGTCATCCCTTCATGCCCCCTTCTTCAAAGGTAAACAGGTTACAGGGCTTCCCTGCCTC	58586	Db	59607	CCCCCGAGTGGCTCTCTACCACTCAGAAAGCCGAGTTTCCCACCTCCACGAGACAGCC	59666
QY	1798	-----	1797	QY	1971	AGTGGCGAGGATTCCACAT	1991
Db	58587	CATCCCTCCATCCCCCTTCCTGCTGCCTCCATCCCCCTTCCCTTCCCTGCCCTCATCC	58646	Db	59667	AGTGGCGAGGATTCCACATGTAAGTGGTGGCGATGGTGGCGAGGAGGGGTG	59726
QY	1798	-----	1797	QY	1992	-----	1991
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QY	1798	-----	1797	QY	1992	-----	1991
Db	58707	TGATGCTCAGGAGTGCAGAGATGAATTAGGAGTTCTTAGACTGGAAGAAAGAAGACAT	58766	Db	59787	CCCGGCCCTTCCATACATGATTTGATAATGTTACGCTCTGTGCTCTGAGCCAGGGGC	59846
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Db	58827	GGAGGGGCAGAGGCAGGGCTCTATGGGGTGAGGTAGGCCCAAGGAGCCGTTATGCC	58886	Db	59907	GAAAGTGGTGGTGGGTGGAGGCAAGAAGCAGATGTGATATGGCTCTTGGAGGGG	59966
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Db	58887	TTACACCTTTCTGGGCTACAGGAGGCGAGAAAGTTTGGGGACCTATGAACAAACCCATCT	58946	Db	59967	AAAGGTTGGTTCCACAAAGGGCATCAGTGCTCCTGACTCTCTCCACCAGGCT	60026
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QY	1864	-----	1863	QY	2235	TGAGCAGGCACTGTGGAGGAGCCATCCCTCTGTATGACTGCGACCTAAGGAGGACCTC	2294
Db	59187	CAGGGTGCCAGCCTCAGAGCTCTACCAATTCAACGAGAGCCCTTCAGCCCTCTTCTCTC	59246	Db	60267	TGAGCAGGCACTGTGGAGGAGCCATCCCTCTGTATGACTGCGACCTAAGGAGGACCTC	60326

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Qy	2424	-----	2423
Db	62607	GACAGAGGAGTCAATTGTTACACACACATCCCCCTCTTCTCTCTCTCCCTCCACTT	62666
Qy	2424	-----	2423
Db	62667	CCCTGTGAAGCCCTGAGCAGGCTGTGGCCAGGCTCAGGCCCTGACTGTGGGTACACAC	62726
Qy	2424	-----	2423
Db	62727	CAGGAGGGCCACGCCCTCCCCACAGACGGGTGGAGTGGTCACTGGAGCCAGCACCTCT	62786
Qy	2424	-----	2423
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Db	63147	GAAACTGAGCAGCAGGAGGTTTGCCCAAGGTACATACTGCTTAATAGCAGGGTAGAC	63206
Qy	2424	-----	2423
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Db	66327	AGACGGAGTCTCTGTTTGGCCAGGCTGGAGTGTGTGTGAGATCTTTGGCTTACTGC	66386
QY	2424	-----	2423
Db	66387	AATCTCCACCTCCCTGGTTCAGCGAATCTCCTGTCTTAGCCTCCCAAGTAGCTGGGATT	66446
QY	2424	-----	2423
Db	66447	ACAGATGTGCATCACCAAGCCAGCTACTTTTTTGTATTTTTTTAGTAGAGATGGGTTTCA	66506
QY	2424	-----	2423
Db	66507	CATGTTGGCAGGGGTCTTGAACTCCTGACCTCAGGTGATCTGCTGCTTGGCTCGGCTCC	66566
QY	2424	-----	2423
Db	66567	CAAGTGTGGGATTACAGCGGTAAAGCCAGCCGCCAGCCACAGAACATTTGTTAACATT	66626
QY	2424	-----	2423
Db	66627	CATTTTTCAGGCTTTTCTTAACCATCTATCTAAATTAAGCCCTTCGTGGCCCTATTTT	66686
QY	2424	-----	2423
Db	66687	TTTTTTAAACAACAACATCTGGCTTATTTATTAGGCACCTGTCTCTAAACCTCTCAAGG	66746
QY	2424	-----	2423
Db	66747	ATTAACATTATCAATCTCACCATAGCCCTCTAAGGTACTCTTACTTGTCTTATTTTAGA	66806
QY	2424	-----	2423
Db	66807	TCTACGGGGAAATTTAGGCACAGAGGGGTGAGGGAACCTTGGCCAGGATTGTACAGCTGG	66866
QY	2424	-----	2423

Db	52432	GGGAGGAGGACAGAGTCAGTACCAGAGTCGGAATAAAGACAGGGTGGGAAGGGAACCTG	52491	QY	1071	TGACAGCCTCGTGAGAGAGGTGATGGCAGCGTTGGCCACAGGAGTGGCTGGACCAAGG	1130
QY	301	AGTCAGGAGACTTGGCTGGCAGCGCTGCCTCCGACGAGAGCGCTGACAGTGGTTCCA	360	Db	53572	TGACAGCCTCGTGAGAGAGGTGATGGCAGCGTTGGCCACAGGAGTGGCTGGACCAAGG	53631
Db	52492	AGTCAGGAGACTTGGCTGGCAGCGCTGCCTCCGACGAGAGCGCTGACAGTGGTTCCA	52551	QY	1131	GGCAGGTGCTGGTGAAGGTCAATTCTGCAGGT	1162
QY	361	TGAACGTGATCCCTGCTGTGGGCTGGGACAGGGCCACTGACACAGTATCGGAGCAGAAA	420	Db	53632	GGCAGGTGCTGGTGAAGGTCAATTCTGCAGGTGGTGGAGTTGTGCCCTGGATAGACCCA	53691
Db	52552	TGAACGTGATCCCTGCTGTGGGCTGGGACAGGGCCACTGACACAGTATCGGAGCAGAG	52611	QY	1163	-----	1162
QY	421	GGGAAAGGACGAGAGGATCCAACTCTGCCAGTTAGCAGCTGTGTGGCTTTGGGCAT	480	Db	53692	AGGAGGTGSCCCTCGGATCTGCGCCAGGTCCCCAGTCAAGATCATTTGTATCATTT	53751
Db	52612	GGGAAAGGACGAGAGGATCCAACTCTGCCAGTTAGCAGCTGTGTGGCTTTGGGCAT	52671	QY	1163	-----	1162
QY	481	GTTACTTAACCTCTCTGAGCCTCATTTATTTTCATCATATAAATGAAATAAAATAATAC	540	Db	53752	GTCACTCTTCTGGTCTTCTCAGTGTGAATGATGGCTAGCATTAATGGGAGGTGGAGTGC	53811
Db	52672	GTTACTTAACCTCTCTGAGCCTCATTTATTTTCATCATATAAATGAAATAAAATAATAC	52731	QY	1163	-----	1162
QY	541	TTTTGTCAAAGGCGCATTTGTGAATATTTAGATCTCAGATAATGCCTGGCTTTGAGCAA	600	Db	53812	GTCTGTTCCGAAGTGCATTTTCATGCAGTGTGTAAGAGCATGAGCTCTGGAGCTGCTGCTT	53871
Db	52732	TTTTGTCAAAGGCGCATTTGTGAATATTTAGATCTCAGATAATGCCTGGCTTTGAGCAA	52791	QY	1163	-----	1162
QY	601	ATGGTAGCTGGAGGAAAGGAGAAACCAAGTCAGCAGCTGAAGGATTTTCATATT	660	Db	53872	GCATTCGSCACCAAGCCCTTTAGCTCACCATCTGTGTCTCTGSCAGGTAATTCATCC	53931
Db	52792	ATGGTAGCTGGAGGAAAGGAGAAACCAAGTCAGCAGCTGAAGGATTTTCATATT	52851	QY	1163	-----	1162
QY	661	AGAACTGCTCTGGACCTATCTGGCAGATGCGAAGCACACACACGAGGGGCGATGAT	720	Db	53932	CTCTGTGCTCAGTTTATCATCCATAAATGGGAATAGTAGAGTACTTGCCTCCTGGAG	53991
Db	52852	AGAACTGCTCTGGACCTATCTGGCAGATGCGAAGCACACACACGAGGGGCGATGAT	52911	QY	1163	-----	1162
QY	721	TTGCCCGCCCTTAGACATGTTGTCTTCTCTGGATCCTTGGTCCAGGTGCCCTACC	780	Db	54052	GTGATACATAAGTATTAGCTGCTATTTATTCATCATTTTGTGTAGTCAATTAATATGA	54111
Db	52912	TTGCCCGCCCTTAGACATGTTGTCTTCTCTGGATCCTTGGTCCAGGTGCCCTACC	52971	QY	1163	-----	1162
QY	781	TGAGCTCAGTGAATGTGGCAGCAGAGCCCTCTGGTGGTGAATGCTGTGGCGCCC	840	Db	54112	ATTAATAACATCTCATGAGATACAGGTACTTTATTCCTATTTTCAGACAAGACACTGA	54171
Db	52972	TGAGCTCAGTGAATGTGGCAGCAGAGCCCTCTGGTGGTGAATGCTGTGGCGCCC	53031	QY	1163	-----	1162
QY	841	GTGCTCTCTGGTACACAGGGACCTCACAAATCCCTCCACGGTCTCTCTCATGTCTT	900	Db	54172	AGCTCAAAGGCGATGAGCTATTCTCAAGCTCACACAGTGAGAGTAGCTGGTCTTGGAAAC	54231
Db	53032	GTGCTCTCTGGTACACAGGGACCTCACAAATCCCTCCACGGTCTCTCTCATGTCTT	53091	QY	1163	-----	1162
QY	901	CCCAGCCTTATTTCTGCTTCTCTTCTCCAGCCCGGAACTTGCCTGTTTGGCTCCC	960	Db	54232	TTAAGTAGTCTTCATTTGTTTGTAGTCACTCAGCAAAACATTTTGTAGGATCAGCTATGAGCC	54291
Db	53092	CCCAGCCTTATTTCTGCTTCTCTTCTCCAGCCCGGAACTTGCCTGTTTGGCTCCC	53151	QY	1163	-----	1162
QY	961	CAACCAGCAGCAGCCCTTCTTGGCAGCAGCTGTGCCATCCAAAGTTGGGGATAA	1014	Db	54292	AGCAATATGTTAGGAGCTGGAGATACACACAGCAGGTAAACAGGTCAAGTTGATGGTTAA	54351
Db	53152	CAACCAGCAGCAGCCCTTCTTGGCAGCAGCTGTGCCATCCAAAGTTGGGGATAA	53211	QY	1163	-----	1162
QY	1015	-----	1014	Db	54352	GAGCATAGCAGGTGGACTCCAGACCCCGTGAAGGCATCTTAGGCTCACCATTTACTAGCT	54411
Db	53212	GTGGTCTGTGCCGGTGGCAGACGCCCGACATCTGCACCCCTGCTCTCTGCCCTCTCTTG	53271	QY	1163	-----	1162
QY	1015	-----	1014	Db	54412	GTGTATGCTGGGCAAGTTGCTTAACCTCTCTGAGCCCTGCATTTTCCCTCACCTGTGATG	54471
Db	53272	TCCTGCTGTGCTGACTTTGACCTCGGTGTGCTTGGGCAAGGTGGCAGCTGTACTCCT	53331	QY	1163	-----	1162
QY	1015	-----	1014	Db	54472	AGGACTGTAATTGTATCTACCCACAGGGTTGCAANTGGCTAAGTGAGCTAATGTGTGTAAA	54531
Db	53332	CAGGCTGTGTTCCAGGCTGCTGGCTAGATCTGCTTCTTCTTGTGCTCA	53391	QY	1163	-----	1162
QY	1015	-----	1014	Db	54532	GCAGTACACAGGCGCTGCCAGTCAGTGTGAGAAACATGGCGGCTCAGGAGTATTAAAG	54591
Db	53392	GGGCTCCCCACCTGCAGCTCAGCCTCTTGGGATCCCTCCACCATTTACTGCAATAGCC	53451	QY	1163	-----	1162
QY	1015	-----	1014	Db	54592	ATGGGCTCCAGAGAAACCTGGAACATTTCAAACCACCTGTCTCTCGGAGGGCAGCGGCT	54651
Db	53452	GCCCTCTCCCTGCGGTGGAGATCAGGAGCCCTTCCCACAGCTCAGTCTGGTCTCCT	53511				
QY	1015	-----AGTCCCTATGACATCTTCCGCGCCAGACCACTAGTGTGACCCCTGCAAGTCCGCTG	1070				
Db	53512	CTTCAGTCCCTATGACATCTGCGGCGCAGACCACTCAGTGTGACCCCTGCAGCTGCTG	53571				

Qy	1163	-----	1162
Db	54652	TGACAGCTGGAACCCAGGCGACAGAAATAGGGCGTTCAAGAAGTGGGATGAGAAA	54711
Qy	1163	-----	1162
Db	54712	AGAAAGCCTTCTCCCTTCAGGAAGTGGGAGAGATGGTCACTGTGTGCCCTGG	54771
Qy	1163	-----	1162
Db	54772	GAAGCACTGCCCTCTGCTGCCACCTGGTGGTTGCAGTTGCCCAAGGTCATGTTATT	54831
Qy	1163	-----	1162
Db	54832	GAGACCTTACTATGTGCCAGGCACGTGTTTAGAGCACTGATCTCCGGAAGCACTTGGATCGA	54891
Qy	1163	-----	1162
Db	54892	CACCCATGTCAATAACCAACATTTAATTTAAACCCACACCCCACTGTGTGAATATTGTT	54951
Qy	1163	-----	1162
Db	54952	TGTAAGTTAATACATATATTACTACATTAATATCATATAAAGATAGATAAAATAGAAA	55011
Qy	1163	-----	1162
Db	55012	TTGATGGAGTAGAAATGCAAAAGCAGGTAGAAAAGTAAACGTAAAGTAGAAGAGCTCATAT	55071
Qy	1163	-----	1162
Db	55072	TTTCCCAAGCACATGGATGATCTGATGTACTTTACTTTGGAGGCCACTGCTCTAGGGAC	55131
Qy	1163	-----	1162
Db	55132	TGGGACTCAAGCACAGTCCCAGTCCATGAGGAGCTGATCAAAATCAACACCAAGGCTTA	55191
Qy	1163	-----	1162
Db	55192	TATAAGACACTTCCCAATTTTCAAGGGCTTTTATACATAGCATGTACTTATAGTACTA	55251
Qy	1163	-----	1162
Db	55252	TTTATATACATATTTTATTTGACTTATGAATAGTTGGGGCAAGTCTTATTTGCTCCAT	55311
Qy	1163	-----	1162
Db	55312	TTTACCAGGAAGTGAAGCTGAGGAGGCTCAGACCCCTGCCCAGGTTCTTCTCTGAC	55371
Qy	1163	-----	1162
Db	55372	TCACTGAGAATCTTTCTCTATCCTCTTGGATGTGCTTCCCTGGGCTGCCGTGGGTGG	55431
Qy	1163	-----	1162
Db	55432	GCATATGCACCTGTGATTTCTGAGCACCAACCCAGGACTTCAACCCCGCTACTAGAGAAA	55491
Qy	1163	-----	1162
Db	55492	CAACCTCTCAGCCTCCAAACAGCACCTCCACCCCTGGCATCCAGCTGGTCCCGGCTCC	55551
Qy	1163	-----	1183
Db	55552	CTCCCTTCCCCCAACCCAGTCCGCTCTGTGTCTTTTGCAGATGCCATTTGGCTTGCAGCCA	55611
Qy	1184	GATGCCCGTGGTGTGCCACATCTCTGGGGCTCAATGAGGCTCTCTTTGTCACACCCA	1243
Db	55612	GATGCCCGGTTGTGCCACATCTCTGGGGCTCAATGAGGCTCTCTTTGTTGTCAACCCA	55671
Qy	1244	CAGGAAGTGCATGAGCT-----	1260
Db	55672	CAGGAAGTGCATGAGCTGTTAGGACCAGGAGGTTGCCAGGGTCCAGGGAGGAGATCTA	55731
Qy	1261	-----	1260

Db	55732	TTTTAGTGTGGCAGTGGTGGATTCTGGGAGGTTCCAGGGAGAGAGGAGGAGGGGC	55791
Qy	1261	-----	1260
Db	55792	CTGGCTCTGGCTGCTGTGGTTCCTCAGCACAAAGGAGTGGGCCCTCAGCTGATGGGG	55851
Qy	1261	-----	1260
Db	55852	AATTCCCAAGATAGTGCAGGGCAGGGGCTGGTAGCACTGGTTGGGAGCTCCCAAGGAGAA	55911
Qy	1261	-----	1260
Db	55912	AGAGGAGACCTGCCCTAGTTAGGGGTTCCCCAGGAGACAGAGAGGCCCAAGAGGGGTC	55971
Qy	1261	-----	1260
Db	55972	TCAGCACTGGGGAGCCCTATCTCCAGCTGCTATAGCCCCCTAGAGACCCCTCTACTCCCA	56031
Qy	1261	-----	1260
Db	56032	CTCCTGCCCTCCCTAACCCCTCCTTAACACGAGCATAGAGTCTTGGCCCCAACCCCTCTCC	56091
Qy	1261	-----	1260
Db	56092	CCCTAACCTCTGCTTTTCCCTGGATTCTCAGGCAGCCCCCTTGAGCACTCTCTCCACCCGC	56151
Qy	1261	-GATCCACACCTTGACCACTGGGGCCCACTGTGGGCTCTGCTGAGGGGCTGGACCTGG	1319
Db	56152	AGATCCACACCTTGACCACTGGGGCCCACTGTGGGCTCTGCTGAGGGGCTGGACCTGG	56211
Qy	1320	TGAGTGGCAAGGACCTTGGCAGGCACTGACGACCACTGAGGCTCTTCAACAGTA	1379
Db	56212	TGAGTGGCAAGGACCTTGGCAGGCACTGACGACCACTGAGGCTCTTCAACAGTA	56271
Qy	1380	TCCA-----	1383
Db	56272	TCCACCAAGTATGGGAGCAGAGCTGGGGGAGGAGACGGCGGGGGCGCCGGGCTCG	56331
Qy	1384	-----	1408
Db	56332	GCTCAGCACTGGCTGACCTCTCTGTGTGACCCCAACCCAGGTGAGCTGATCTGATGTG	56391
Qy	1409	CTGGGGCCCCCAGCATCTGCGGGATGTCAACACCGCCCAACCTGGAGCGCTTCATGCGCGC	1468
Db	56392	CTGGGGCCCCCAGCATCTGCGGGATGTCAACACCGCCCAACCTGGAGCGCTTCATGCGCGC	56451
Qy	1469	TTCAATGAGCTGCACTGCTGGTGGCCACCGAGCTGTGTCTGTGCCCCCGTGGCGGCCCC	1528
Db	56452	TTCAATGAGCTGCACTGCTGGTGGCCACCGAGCTGTGTCTGTGCCCCCGTGGCGGCCCC	56511
Qy	1529	CGGGCCCCAGCTGCTCAGGAAGTTCAATTAAGCTGGCGGCCA-----	1569
Db	56512	CGGGCCCCAGCTGCTCAGGAAGTTCAATTAAGCTGGCGGCCCAAGTAGTGTCTGTCCAGTGG	56571
Qy	1570	-----	1569
Db	56572	GTAGGGCTGGCCAGAGTCCCGCGCTACTTTTCTTAAGCCCCCTCTTTGCTTAGTA	56631
Qy	1570	-----	1569
Db	56632	TGTTGCCAAATCTGCCACCCCTATTGTTTCCCTGGTCCCTGGAGGCTCTGTCCCTCCAC	56691
Qy	1570	-----	1569
Db	56692	CCCATCCAGCTTGGATCTCTGACAGAGGCTGGCCTGGCTGTTGTCTGGGGGCACTGTAGGG	56751
Qy	1570	-----	1582
Db	56752	GTGGCTGCTTCCCTTACCCTTGAGGGTCTCTGGGTCTTCTGCTCACAGCCCTCAAGGAGCAG	56811
Qy	1583	AGAAATCTCAATTTCTTCTTTGGCGTCATGTTTGGCGCTCAGCAACTGCGGCCATCAGCCGC	1642

Db	56812	AAGAACTCAATCTCTCTTTGCCGTCATGTTTGGCCCTCAGCAACTCGGCCATCAGCCGC	56871	QY	1711	-----GGATCCCTCATGGAACCAACCGGGTATACCGACTGGCCCTCGCCAAGCTC	1759
QY	1643	CTAGCCACACTCTGGG-----	1658	Db	57952	TTCTCCCTCCTAGGATCCCTCATGNAACCAACCGGGTATACCGACTGGCCCTCGCCAAGCTC	58011
Db	56872	CTAGCCACACTCGGAGGTAAAGTGTGTCTGGAGGGCCCCCTCCTGAGGTCAAGCCCTCA	56931	QY	1760	TCCTCTCCTGTATCCCTTTCATGCCCTTCTCTCTCAA-----	1797
QY	1659	-----	1658	Db	58012	TCCTCTCCTGTATCCCTTTCATGCCCTTCTCTCTCAAAGGTAAACAGGGCTTCTCTGCCTC	58071
Db	56932	GGCCCTCCTGGAGTGTGGATGGGCTGGGCTCCCCAGAGCAGCCGCTCATCTGCCT	56991	QY	1798	-----	1797
QY	1659	-----ACGGCTGCTCACAAGTCCCGAAGCTGTACTCCGCCCTCGAGAGGCTGC	1709	Db	58072	CATCCCTCCATTCCCCCTTCTCTGCTCCATCCCCCATTTCCCTTCTCTGCTCCATCC	58131
Db	56992	CCTTTTACAGCGGCTGCTCACAAGTCCCGAAGCTGTACTCCGCCCTCGAGAGGCTGC	57051	QY	1798	-----	1797
QY	1710	T-----	1710	Db	58132	CCCATCCCATGCCTATCTGTGTGTGCCACCCACTCTGTGGAGAGATTATACCTCAAGTGC	58191
Db	57052	TGGTGAGTGTCCACCTTGCCCGGCTGGCTGTCTGTAGGATCAGTGGGCTCGGCCCTGC	57111	QY	1798	-----	1797
QY	1711	-----	1710	Db	58192	TGATGCCCTCAGGAGTGCAGAGATGAATTAGGAGTTCTTAGACTGGAAGAAATGAAGACAT	58251
Db	57112	CCTCCAGACACCTCAGCTTTGGCTTCCCTGCAGCCCTCTACTCGTCTTTGTCACTTT	57171	QY	1798	-----	1797
QY	1711	-----	1710	Db	58252	CCAGACAAATACGGGCTGCCCTTTCAGGGCCTTAAGAGATACAAGAAATCTGCTGGGGCTT	58311
Db	57172	CAGGTTCCCAACCTCGGCCCAAGGCTAGCTCCAGCCTGTAGTTTGGGAGCTGGCTG	57231	QY	1798	-----	1797
QY	1711	-----	1710	Db	58312	GGAGGGGCACAGCAGGGGCTCTATGGGTTGAGTAGGCCAAGGAGCCGTTATGCC	58371
Db	57232	AGGAAGGGTGTTCAGCACTAGGATAGGGTTGCACGGTGCATCCTGCCCTCAGTGTGT	57291	QY	1798	-----	1797
QY	1711	-----	1710	Db	58372	TTCACTTTTCTGGGCTACAGGAGGGCAGAAAGTTTGGGAGCTATGAACAAAACCATCT	58431
Db	57292	GCATGGGGCAGGAGATCCTGTGTGAAGACTGGGCTGGAGCATGTGGGTGCCAGTCTG	57351	QY	1798	-----AGACATGACCTTTCATTCATGAGGAAACACACACTAGTGGAGATCTCATCAA	1851
QY	1711	-----	1710	Db	58432	CTTTGCACATGACCTTTCATTCATGAGGAAACACACACTAGTGGAGAAATCTCATCAA	58491
Db	57352	GGTCTGAGTGCACAGGCTGTCTAGGGGCTCCAGAGCCCAAGGGCTCGCATGGAGCG	57411	QY	1852	CTTTGAGAAGAT-----	1863
QY	1711	-----	1710	Db	58492	CTTTGAGAAGATGGTGTGAGTCCAGGAGAGCAGGCATTCTACTTAACATAGTTGGAGGA	58551
Db	57412	CCTGTGTGCACAGGGCTGTCTGCCCTCAGGAACCTCCAGGGCTTCCGGGCTAGACC	57471	QY	1864	-----	1863
QY	1711	-----	1710	Db	58552	CATGACTGTGGCTGGGAAGGGCAGGGCTTGGAGCAGCTTAAACTTGTATGAATAAT	58611
Db	57472	AGTAGAAGGCGAGGATAGAGTTGGGGTGGAACTCCACCTCCAGGAATTTTGAGG	57531	QY	1864	-----	1863
QY	1711	-----	1710	Db	58612	ATGAGGATGAATACTTACTGTGTATAGCCCTTGCCTTATTCCTGCTGCACTGGGCTGTC	58671
Db	57532	ATTTTGAGGGTTTGTACTATTCTGGAGAGAAGCAGAGAAGAGGTACTTTCATCAGCATAGC	57591	QY	1864	-----	1863
QY	1711	-----	1710	Db	58672	CAGGTGCCAGCCTCAGAGCTCTACCATTCACACGAGAGCCCTTCCAGCCCTCTCTCTCTC	58731
Db	57592	CTGGAGCTCTTGAGAGAAATCCACCTCTGTTGGGCTCAAGGGATTCAAGGAGTTTACT	57651	QY	1864	-----	1863
QY	1711	-----	1710	Db	58732	TAAGCTTTCTCTCTGGCCTCTGCCTTCTGTCTCTGCTGCTCCCGCTGGGCTCTGT	58791
Db	57652	CTCAGAGAGAGAGGGGAGGACACAGAAAGACAGAGAGGATAGAAAGGACAGAGAGGT	57711	QY	1864	-----	1863
QY	1711	-----	1710	Db	58792	GGTGTGTGAGGGAAGTACACATGATGCCACATTAACCAAGGATCTTACAGTCCCTGATC	58851
Db	57712	GACAGTGACAGACTTTTCCAAGAAACCTGGGGGCCCTGTGACTAACTGCTGTGAATTTTC	57771	QY	1864	-----	1863
QY	1711	-----	1710	Db	58852	CTTGGTTCAGAGGGAGCTTGGCCCTCCCTGCTGCTGCACAGGCGCAGGAGGGTTTCTCCC	58911
Db	57772	TCAGTGCTAATGGAGGTTGGAAGCCCGTGTTCGCCCTGTACAGAGCCTGGGTGAGACC	57831	QY	1864	-----GAGAAATGATGCCAGAGCCGCGGA	1889
QY	1711	-----	1710	Db	58912	TCAGCAAGAGCTTATGCCCGGTGTGTCTCCGACAGAGAATGATGCCAGAGCCGCGGA	58971
Db	57832	TGGGCTGAGGAGGCTGAGTTGGGGCTCTGCACCTGCTGTGGATGGGCATGTGCC	57891	QY	1890	TGCTGCACCACTCGGGAAGCCACACCTT-----	1918
QY	1711	-----	1710	Db	58972	TGCTGCACCACTCGGGAAGCCACACCTTGTGTGAGAGGGGGTCCCGGGGTGGAGGT	59031
Db	57892	CCTCCTTGGTTGGGCTGTGTGGCTTATGTGTGTGCAACCCCTCAGTGTGGC	57951				

QY	1919	-----	1918	
Db	59032	CCCCACCCATACATCTCTGTGAGGCTCCAGGCTGGCCCTGACTCCATGACCCCTCCCCA	59091	
QY	1919	-----GTGCGCTCTCTACCACTCAGAAAGCCGAGTTTCCCACTTCCACGAGGACAGCC	1970	
Db	59092	CCCCCGAGTGCCTCTCTACCACTCAGAAAGCCGAGTTTCCCACTTCCACGAGGACAGCC	59151	
QY	1971	AGGTGGCGAGATTTCACAT-----	1991	
Db	59152	AGTGGCGAGATTTCACATGTAAGTGTGGCGATGGTGGTGGCGAGGAGGGGGTG	59211	
QY	1992	-----	1991	
Db	59212	CTTATGTAGTTACCCATGSGCTGGCACATCTTAGGCACCTTGCCATGTGCCAGCACGGAG	59271	
QY	1992	-----	1991	
Db	59272	CCCGGCCCTTCCATACATGATGTTGATAATGTTACGCCCTCTGTCTCTGAGCCAGGGGGC	59331	
QY	1992	-----	1991	
Db	59332	TCCTTCGGTCCCCTCACCCGTGGGGTGGCGAGGACAGCCGCTTTTAGGAATTGGTGATGG	59391	
QY	1992	-----	1991	
Db	59392	GAAGTGTTGGTGGTGGAGGGCAAGAAGGCAGATGTGATAGCTCTTGGAGGGG	59451	
QY	1992	-----GCT	1994	
Db	59452	AAAGTTGGGTTCCAAAGGGGCATCAGTGCCTCCCTGACTACTCTCTCCACCAAGGCT	59511	
QY	1995	CGGAGCAGTCCCTGAGCACCCGAGTCCAGCCAGCACCTGGGCTTATGTCCACGACCTGA	2054	
Db	59512	CGGAGCAGTCCCTGAGCACCCGAGTCCAGCCAGCACCTGGGCTTATGTCCACGACCTGA	59571	
QY	2055	AGGTCAATTGACAAACCGGGAACTCTCCCGCTCTCCGAGAGCTGGAGCCATGAGGAG	2114	
Db	59572	AGGTCAATTGACAAACCGGGAACTCTCCCGCTCTCCGAGAGCTGGAGCCATGAGGAG	59631	
QY	2115	GGCTGGGACTGGAGCTGGAGCAGGCACTTGACCCGGGAAAGCCAGGCTGTGCCGGCC	2174	
Db	59632	GGCTGGGACTGGAGCTGGAGCAGGCACTTGACCCGGGAAAGCCAGGCTGTGCCGGCC	59691	
QY	2175	AGATACTCACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGTGGAGTGGACTCGAGTCCC	2234	
Db	59692	AGATACTCACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGTGGAGTGGACTCGAGTCCC	59751	
QY	2235	TGGAGCAGCAGTGGAGGCGCCATCCCTGTGTGATGACTGGCAGCTAAGGAGGACCTC	2294	
Db	59752	TGGAGCAGCAGTGGAGGCGCCATCCCTGTGTGATGACTGGCAGCTAAGGAGGACCTC	59811	
QY	2295	GGAGTGGACCCGAGCCAGGAATAACGAATGACCAAGGCCAAGGAGGAGGACAGAGAG	2354	
Db	59812	GGAGTGGACCCGAGCCAGGAATAACGAATGACCAAGGCCAAGGAGGAGGACAGAGAG	59871	
QY	2355	GGCCAGGAGTGGGTGGAGAGTGGAGTGGCGCTGGGACGTTGTGTGCAATAGAGAGTCTC	2414	
Db	59872	GGCCAGGAGTGGGTGGAGAGTGGAGTGGCGCTGGGACGTTGTGTGCAATAGAGAGTCTC	59931	
QY	2415	CACACCAGA-----	2423	
Db	59932	CACACAGATGCTTTCCAGATTCTGTGCCTCTGGCTTTTGTGTCCAGCCAGGCTGCAGT	59991	
QY	2424	-----	2423	
Db	59992	TTATTTTACAGTGGACAGAGAGAGAGAGGCTGCATGTGTACCGTGTGTGGCAA	60051	
QY	2424	-----	2423	
Db	60052	GGCAGGGCTTGGCTGGGCGAGGGGCCCTGCTTTCTTCCACAGCTTTCTTCCAAC	60111	
QY	2424	-----	2423	

Db	61192	GCCTCAGTTAGGGCTGAGGAGAGACTCAGGTGCAGCAGATGCGAGTGGTAACCAACC	61251	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62332	AAAGGAAGGCAGAGCCTGAGATCGGCGACCCCATCCCCCTCCACTCAGCACTGAGTTAG	62391
Db	61252	AGTTCCCTTGCCGTGGGTGGGACACAGGAGAACGACGACATCTGGAATGAGCAAT	61311	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62392	AGCTGGTGGGGCATGTCTGCTTCACACGCTGCTTATGGCTTCCTGTGTCTCCAACAG	62451
Db	61312	CAGGACAGAGGCTCAAGCCTGGGTGAGTCAGAGTCGGGGGCTTCTTTTCATCCAAC	61371	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62452	CCCTCAGCCTCTGGTGTCTCTTCCTTCCTCAATAGTCACAAGATTTACCATGATAAATAG	62511
Db	61372	CCATTGTCTGTGTGTCTCGGCAAAAGCCAGCCAGCCGCTGGCCCTTCCACGGTCT	61431	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62512	GTTAAGACTTGAATGGTGTTCATCTCTTCATCTTCACCCCTGCTCAGCTTAGGTTA	62571
Db	61432	TCAGACTTAGGGTAGCCAGCCAGCGACGACACACAGAAACCAAGTGCACGGGGCGG	61491	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62572	TTTTTATCTGTATGACAGATAGGTACTACAGGTATTTTACTCTGGTTTACAGTCAAA	62631
Db	61492	GTGTCTCCACCAGCATTTCTCTCTGTGTCACATCTAGTCTCTGATGGACTTCTCCCTC	61551	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62632	CAAACTGAGGCACAGCAGGTTTGCCCAAGGTCACATAACTGCTTAATAGCAGGTAGAC	62691
Db	61552	CTCCTTGACCATCAGCTTTACAGTCCAGACCACCTGCAGCACCCGCTGGTCTCCAG	61611	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62692	AGGTGAAGTAACTGGATGTGTATCAGCCATGCCCTTTCCCCATGCCCGGCACTCCCA	62751
Db	61612	CTGCCCACTCTCGGGCAGGATGGCTTTTGAGCCTGTGGGAGAGACCTTGCCAGAGAA	61671	Qy	2424	-----	2423
Qy	2424	-----	2423	Db	62752	TCAGACGCTCTGTAATCCCAACATTTATCTTTTCAGGATTTAGACCAAGCATATAAA	62811
Db	61672	TGGTGCCAGGCAGCAAGAGACAGACTCTGGGAGCTAGAGAGTTGGCGCCAGG	61731	Qy	2424	-----	2423
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LOCUS Homo sapiens, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.
DEFINITION AC004241
ACCESSION AC004241
VERSION AC004241 GI:3004524
KEYWORDS HTG: HTGS, PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
Muzny,D., Arenson,A.D., Brundage,E., Carvelli,K., Chen,E., Di,W.,
Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesh,R., Garcia,C.,
Goodman,M., Gorrell,J.H., Haywood,M., Jackson,L., Kampal,R.,
Karpathy,S., Leal,B., Li,Y., Liu,W., Logan,O., Lu,J., Ly,T.,
Martinez,C., Oswal,G., Perez,L., Rashid,N.D., Rowland,K.,
Savage,L., Scherer,S.S., Shen,H., Timms,K.M., Todd,J., Vo,Q.,
Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.
Direct Submission
Unpublished
JOURNAL 2 (bases 1 to 158111)
REFERENCE Worley,K.C.
AUTHORS Direct Submission
TITLE Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor
JOURNAL College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT [WARNING] On Apr 4, 1998 this sequence was replaced by a newer
version gi:3023023.
On Apr 1, 1998 this sequence version replaced gi:2995474.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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* as soon as it is available and the accession number will
* be preserved.

1		52081: contig of 52081 bp in length
*	52082	52101: gap of unknown length
*	52102	52083: contig of 40792 bp in length
*	92894	92913: gap of unknown length
*	92914	132793: contig of 39880 bp in length
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*	154291	154310: gap of unknown length
*	154311	155295: contig of 985 bp in length
*	155296	155315: gap of unknown length
*	155316	156019: contig of 704 bp in length
*	156020	156039: gap of unknown length
*	156040	156741: contig of 702 bp in length
*	156742	156761: gap of unknown length
*	156762	157448: contig of 687 bp in length
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Best Local Similarity		16.2%; Pred. No. 4.5e-126;
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QY	61	GGGGTTTTGAGACCAGGGTTTTGGAAGAGAGTTTCAGCACTGCTGGTAGTTTTGGGAATCA 120
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QY	121	CCCATGTGACGGGCACATAGGGCAGTAAGGAACTCTCGAGGGGTCCCTGAGATTGGA 180
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Db	56007	CAAGCTCTCAGCTCCCAACAGACACCTCCACCCTGGCATCCAGTGTGCCCGGCTCC	56066
Qy	1163	-----GATGCCATTGGCTTCGACGCA 1183 	
Db	56067	CTCCCTCCCCCAGCCAGTCCGCTCTGCTCTTTTGCAGATGCATTTGGCTTCGACGCA	56126
Qy	1184	GATGCCCTGGTGGCCACATCTCTGGGGCTCAATGAGCGTCTCTTTTGTGTCAACCCA	1243
Db	56127	GATGCCCTGGTGGCCACATCTCTGGGGCTCAATGAGCGTCTCTTTTGTGTCAACCCA	56186
Qy	1244	CAGAAATGCATGAGCT----- 	1260
Db	56187	CAGAAATGCATGAGCTGGTAGGACCAGGAGGGTGGCAGGGGCCAGGGAGGAGATCTA	56246
Qy	1261	-----	1260
Db	56247	TTTTGAGTGTGGCAGTGGTGGATTCTGGGGAGGGTCCCAGGGAGAGAGGAGGGGGC	56306
Qy	1261	-----	1260
Db	56307	CTGGCTCTGGCTGCTGCTGGGTCTCTCAGCACACAAAGGAGTGGGCTTCAGCTGATGGGG	56366
Qy	1261	-----	1260
Db	56367	AATTTCCCAAGATAGTGCAGGCGAGGGGCTGGTAGCACTGGTTGGGAGCTCCCAAGAGAA	56426
Qy	1261	-----	1260
Db	56427	AGAGGAGACCTGCCCTAGTTAGGGGTTTCCCGAGGAGACAGAGCCCCAAAAGGAGGGGTC	56486
Qy	1261	-----	1260
Db	56487	TCAGCACTGGGGAGCCCTATCTCCAGCTGCTATAGCCCTATAGACCCCTCTACTCCCCA	56546
Qy	1261	-----	1260
Db	56547	CTCCTGCCCTCCTAACCCTCCTCTTAACACGAGCATAGAGTCTTTGCCCAACCCCTCTCC	56606

QY	1261	-----	1260
Db	56607	CCCTACCTGTGCTTTCCCTGATTCTCAGGAGCCCCCTGAGCACTCTCCACCCGC	56666
QY	1261	-GATCCACACCTGACCACTGGGCCCACTGTGGCTCTGTGAGGGCTGACCTGG	1319
Db	56667	AGATCCACACCTGACCACTGGGCCCACTGTGGCTCTGTGAGGGCTGGACCTGG	56726
QY	1320	TGAGTGCACAGGACCTGGCAGGCGAGCTGACGACCAACGACTGGAGCCTCTTCAACAGTA	1379
Db	56727	TGAGTGCAAGGACCTGGCAGGCGAGCTGACGACCAACGACTGGAGCCTCTTCAACAGTA	56786
QY	1380	TCCA-----	1383
Db	56787	TCCACCAGGTATGGGAGGACAGCTGGGGGAGGAGACAGCGCGGGCGCCCGGCTCG	56846
QY	1384	-----CCAGGTGAGCTGATCCACTATGTG	1408
Db	56847	GCTCAGCACTGCTGACCTCTCTGTGACCCACCGCAGGTGAGCTGATCCACTATGTG	56906
QY	1409	CTGGGCCCCCAGCATCTGGGGGATGTACACACCGCAACCTGGAGCGCTTCATGCGCGC	1468
Db	56907	CTGGGCCCCCAGCATCTGGGGGATGTACACACCGCAACCTGGAGCGCTTCATGCGCGC	56966
QY	1469	TTCAATGAGCTGCAGTACTGGGTGGCCACGAGCTGTGTCTGTGCCCCGTGCCCCGCC	1528
Db	56967	TTCAATGAGCTGCAGTACTGGGTGGCCACGAGCTGTGTCTGTGCCCCGTGCCCCGCC	57026
QY	1529	CGGGCCAGCTGCTCAGGAGTTCATTAAAGCTGGCGGCCCA-----	1569
Db	57027	CGGGCCAGCTGCTCAGGAGTTCATTAAAGCTGGCGGCCCAAGTGCCTGTGCCAGTGG	57086
QY	1570	-----	1569
Db	57087	GTAGGGCGTGGCAGAGTCCCCCGGTACCTTTTCCTAAGCCCCCTCTTTCCTTAGTA	57146
QY	1570	-----	1569
Db	57147	TGTTGCCAAATCTGCCACCCATTTGTTCCCTGGGTCCCTGGAGCCTCTGCCTTCCAC	57206
QY	1570	-----	1569
Db	57207	CCATCCAGCTTGGATCTCTGCAGAGGCTGGCCTGGCTGTGTCTGGGGCACTGTAGGG	57266
QY	1570	-----CCTCAAGGAGCAG	1582
Db	57267	GTGGCTGCTTCCCTTACCCTGAGGGTCTCTGGGTCTTCTGCTCACAGCCTCAAGAGCAG	57326
QY	1583	AGAATCTCAATTCCTTTTGGCGTCATGTTGGCCTCAGCAACTCGGCCCATCAGCCGC	1642
Db	57327	AGAATCTCAATTCCTTTTGGCGTCATGTTGGCCTCAGCAACTCGGCCCATCAGCCGC	57386
QY	1643	CTAGCCCAACACCTGGG-----	1658
Db	57387	CTAGCCCAACACCTGGGAGGTAAGTGTGGTCTGGAGGGCCCCCTCTCTGAGGCTCAGGCCTCA	57446
QY	1659	-----	1658
Db	57447	GGCCCTCTGGGAGTCTGATGGGCTGGGCTCTCCCGCAGAGCAGCCGCTCATCTGCCT	57506
QY	1659	-----AGGGGTGCTCACAAGTCCGGAAGCTGTACTCCGCCCTCGAGAGGCTGC	1709
Db	57507	CCTTTTCAGAGGGGTGCTCCTCAAAAGTCCGGAAGCTGTACTCCGCCCTCGAGAGGCTGC	57566
QY	1710	T-----	1710
Db	57567	TGGTGAAGTCTCCACCCTCCCGGCTGGCTCTGTGTAGATCAGTGGGCTCGGCCCTGC	57626
QY	1711	-----	1710
Db	57627	CCTCCAGACACCTCCTCTTGGCTTCCCTGCGAGCCCCCTCTACTCGTCCCTTTGTCACTTT	57686
QY	1711	-----	1710
Db	57687	CAGGTTCCCAACCTCGGCCCAAGGCTAGCTCCAGCTGTGAGTTTGGGAGCTGGCTG	57746
QY	1711	-----	1710
Db	57747	AGGAAGGGTGTTCAGCACTAGGATAGGGGTTCACGGTGCATCTCGGCCCTCAGTGTGT	57806
QY	1711	-----	1710
Db	57807	GCATGGGGCAGGAGATCTCTGTGAAGACTGGGCTGGAGCATGTGGGTCTCCAGTCTCTG	57866
QY	1711	-----	1710
Db	57867	GGTCTGAGTGCAGGGCAGTGTGAGGGGCTCCAGAGCCCCAAGGGCTGGCATGGAGCG	57926
QY	1711	-----	1710
Db	57927	CCTGTGTGCACAGGGCTCTGTGCCCCCTCAGGAATCTCCAGGGGCTTGGGGCTAGACC	57986
QY	1711	-----	1710
Db	57987	AGTAGAAGGCCGAGGATAGAGTTGGGGTGGAACTCCACCTCCAGGAACCTTTTGAGG	58046
QY	1711	-----	1710
Db	58047	ATTTGAGGGTTTTGACTATTTCTGGAGAGAAGCAGAGAGGTACTTTCATCAGCATAGC	58106
QY	1711	-----	1710
Db	58107	CTGGGAGCTCTTGAGAGAAATCCACTCTGTGGGGCTCAAGGATTCAAAGGAGTTTACT	58166
QY	1711	-----	1710
Db	58167	CTGCAGAGAGAGAGGGGGACACAGAAAGACAGAGGATAGAAAGGACAGAGAGGT	58226
QY	1711	-----	1710
Db	58227	GACAGTGACAGACTTTTCCAAAGAACTGGGGCCCTGTGACTAAGTGTGTAATTTTC	58286
QY	1711	-----	1710
Db	58287	TCAGTGTCTAATGGGAGGTTGGAAAGCCCCGTGTTGCTGTGCAGAGAGCCTGGGTGAGACC	58346
QY	1711	-----	1710
Db	58347	TGGGGCTGAGGAGAGGCTGAGTTGGGGCTCTCCACTCTGTGGGATGGGCATGTGGCC	58406
QY	1711	-----	1710
Db	58407	CCTCCTTGGTTGGGTGGGTCTGTGTGGCTTATGGTGTGTGCAACCCCTCAGTGTGGC	58466
QY	1711	-----GGATCCCTCATGAACCAACCGGTATACCGACTGCGCTCGCCCAAGCTC	1759
Db	58467	TTCTTCCCTCATGCTCCCTCATGGAACCAACCGGTATACCGACTGCGCTCGCCCAAGCTC	58526
QY	1760	TCCCTCTCTGTATGCTCCCTTCATGCCCCCTCTCTCTCAAA	1797
Db	58527	TCCCTCTCTGTATGCTCCCTTCATGCCCCCTCTCTCTCAAAAGGTAACAGGGCTTCTCGCTC	58586
QY	1798	-----	1797
Db	58587	CATCCCTCCATTCCCCCTTCTGCTCCATCCCCCATTTCCCTTCTGCTCCATCC	58646
QY	1798	-----	1797
Db	58647	CCCATCCCATGCTATCTGTGTGTGCACCCACTCTCTTGTGAGAGAGATTATACCTCAAGTGC	58706
QY	1798	-----	1797
Db	58707	TGATGCTCAGGGAGTGCAGAGATGAATTAGGAGTTCTTAGACTGGAGAATGAAGACAT	58766
QY	1798	-----	1797

Db	58767	CCAGACAAATACGGGCTGCCTTACGGGCTTAAGAGATACAAGAAATGCTGCTGGGGCTT	58826
Qy	1798	-----	1797
Db	58827	GGAGGGGCAGAGCAGGGGCTCTATGGGGTAGGTAGGCCCAAGGGAGCGCTTATGCCC	58886
Qy	1798	-----	1797
Db	58887	TTACCTTTTCTGGGCTACAGAGGGCAGAAAGTTTGGGACCTATGAACAAAACCCATCT	58946
Qy	1798	-----	1851
Db	58947	CTTTGCACACATGACCTTCTATTCATGAGGAAACACACACTAGTGGAGAATCTCATCAA	59006
Qy	1852	CTTTGAGAAGAT-----	1863
Db	59007	CTTTGAGAAGATGGTAGCTCCAGGGAGACGAGCAATTCACCTACTAACATAGTTGGAGGA	59066
Qy	1864	-----	1863
Db	59067	CATGACTGTGGCTGGGAAGGGCAGGCTTGGAGGCAGCTTAAACTTGTATGAATAAT	59126
Qy	1864	-----	1863
Db	59127	ATGAGGATGAATACTTACTGTATATAGCCCTTGCCTTATTCCACTGCAACTGGGTCTGC	59186
Qy	1864	-----	1863
Db	59187	CAGGTGCCAGCTCAGAGCTCTACCAATTCACGAGAGCCCTTCCAGCCCTCTTCTCTC	59246
Qy	1864	-----	1863
Db	59247	TAAGCCTTTCTCTCGCCTCTGCTTCTGTCTCTGCTGCTCCCGCTGGGCTCTG	59306
Qy	1864	-----	1863
Db	59307	GGTGTGCTGAGGCGAAGTACACATGATGCCACATAACCAAGGATCTTACAGTCCCTGATC	59366
Qy	1864	-----	1863
Db	59367	CTTGGTTACAGGGAGCTTGGCCTCCCTGCTGCTGCACAGGGCAGGAGGTTTCTCCC	59426
Qy	1864	-----	1889
Db	59427	TCAGGCAAGAGCTTATGCCCGGTCTTGTCCGACAGAAATGATGCCAGAGCGCGCGGA	59486
Qy	1890	TCCTGCACCACTGCCGAAGCCACACCTT-----	1918
Db	59487	TGCTGCACCACTGCCGAAGCCACACCTTGTGTGAGAGGGCGGGTCCCGGGGTGGGAGGT	59546
Qy	1919	-----	1918
Db	59547	CCCCACCTTACATCCTCTGTGAGGCTCCAGGGTGGCCCTGACTCCATGACCCCTCCCGA	59606
Qy	1919	-----	1970
Db	59607	CGCCGCGAGTGCCTCTCACACCTCAGAAAGCCGAGTTTCCACCTCCACGAGGACGCC	59666
Qy	1971	AGGTGGCAGGATTTCCACAT-----	1991
Db	59667	AGGTGGCGAGGATTTCCACATGTAAAGTGGTGGCGATGGTGGTGGGAGGAGGGGTG	59726
Qy	1992	-----	1991
Db	59727	CTTATGGTAGTTACCCATGGCTGGCACATCTCTAGGCACTTGCCATGTGCCAGGCAGGAG	59786
Qy	1992	-----	1991
Db	59787	CCCGCCCTTCCATACATGATCTTGATAATGTTCAGCCCTCTGTGCTCTGACCGAGGGGC	59846
Qy	1992	-----	1991
Db	59847	TCCTTGGTCCCTCACCCGTGGGTGGCAGGAGGAGCGGCTCTTTAGGAATTTGGTATGG	59906
Qy	1992	-----	1991
Db	59907	GAAGTGGTTGGTGGTGGAGGCAAGAAGGCAGATGTGATATGGCTCTCTTGGAGGGG	59966
Qy	1992	-----	1994
Db	59967	AAAGTTGGTTTCCACAAAGGGCATCAGTGCCTCCCTGACTACTCTCTCCACCAGGCT	60026
Qy	1995	CGGAGCAGTCCCTGAGCACCCGGAGTCCAGCCAGCACCTGGGCTTATGTCCAGCAGCTGA	2054
Db	60027	CGGAGCAGTCCCTGAGCACCCGGAGTCCAGCCAGCACCTGGGCTTATGTCCAGCAGCTGA	60086
Qy	2055	AGGTCAATGACAAACAGCGGGAACCTCTCCGCTCTCTCCGAGAGCTGGAGCATGAGGAG	2114
Db	60087	AGGTCAATGACAAACAGCGGGAACCTCTCCGCTCTCTCCGAGAGCTGGAGCATGAGGAG	60146
Qy	2115	GGGTGGGACTGGAGCTGGAGCAGGCACTTGACGCCGGGAAGCAGAGGCTGTGCGGGCC	2174
Db	60147	GGGTGGGACTGGAGCTGGAGCAGGCACTTGACGCCGGGAAGCAGAGGCTGTGCGGGCC	60206
Qy	2175	AAGTACTACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGTGGAGTGGACTCGAGTCCC	2234
Db	60207	AAGTACTACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGTGGAGTGGACTCGAGTCCC	60266
Qy	2235	TGGAGCAGGCACTGTGGAGCAGGCACTCCCTGTGATGACTGGCAGCTTAAGGAGGACCTC	2294
Db	60267	TGGAGCAGGCACTGTGGAGCAGGCACTCCCTGTGATGACTGGCAGCTTAAGGAGGACCTC	60326
Qy	2295	GGAGTGGACCCGAGCAGGAATAACGAATGACCCAAAGCCAAAGGAGGAGGACAGAGAG	2354
Db	60327	GGAGTGGACCCGAGCAGGAATAACGAATGACCCAAAGCCAAAGGAGGAGGACAGAGAG	60386
Qy	2355	GCCCAGAGTGGGTGGAGTGGAGTGGGCTGGGAGCTTGTGCAATAGAGAGTCTC	2414
Db	60387	GCCCAGAGTGGGTGGAGTGGGAGTGGGCTGGGAGCTTGTGCAATAGAGAGTCTC	60446
Qy	2415	CACACAGA-----	2423
Db	60447	CACACAGATGCTTCCAGATTCGTGCTCTGGCTTGTGTCAGCCAGGCTGCAGT	60506
Qy	2424	-----	2423
Db	60507	TTATTTTTCACAGTGGACAGAGAGAGAGAGAGGCTGCATGTGTACCGTGTGTGGCAA	60566
Qy	2424	-----	2423
Db	60567	GGCAGGCTTGGCCTGGGGCAGGGGCCCTGCTTTCTTTCACAGCTTCTTTCACAC	60626
Qy	2424	-----	2423
Db	60627	AGCAGGCACTGGGCTGGGGCTGTGCGGTGGTCCCTGAGGAGCTTTATTTGTTACTGTC	60686
Qy	2424	-----	2423
Db	60687	AACATAGTAGTATGTTCCAGGCCAGCCAGAGTGGGCGTGGCAGGGAGGCTGAGGCCCG	60746
Qy	2424	-----	2423
Db	60747	CCCTCTGGGAAGGAGCTGTGGAGGAGAAAGACGCCCTTGTGCGCACGGGCCAGACTGG	60806
Qy	2424	-----	2423
Db	60807	TCCAAGATCTGTATGCCACCCAGATGTGCTCCAGGGCTCTGGCCAAAGGGGGGCTGGA	60866
Qy	2424	-----	2423
Db	60867	GCCTGGAGCCCTGTTCAGACGCCAGGCTGACCATCAGCTCCCCGTGGTGGTCCAAT	60926
Qy	2424	-----	2423
Db	60927	AGGACTTTTACATCCAGATGCAACTGACAGCTTCTTCCCAACTCCCGCTTTTCC	60986

QY	2424	-----	2423
Db	60987	ACACTTGAGCTCGCTCGCTGCTGGGCCAGGCTTCTGGGGTCTTCTGGGGTGGCTTG	61046
QY	2424	-----	2423
Db	61047	TGATAGAAACAATGCTGAAGCTTCCGGGGAGAGCCCGTCGCTGTTGAGGCCCAACAGAC	61106
QY	2424	-----	2423
Db	61107	TTCCAGGAATCAGGGTTTATCATCAGTGTGAGAAATGGTCCAGCAAGCTCTGGTCATA	61166
QY	2424	-----	2423
Db	61167	CGAAGTCTCTCTTCCCTGCCCCCTTCAGCACTTCCCTAGGAACAGCTACTGCCAGGAC	61226
QY	2424	-----	2423
Db	61227	GCCTCTTGGAGGCAGAGCTCACCCAGGAAGCTCCAGGGACTCCACCCCTCTTGCCTTGCT	61286
QY	2424	-----	2423
Db	61287	ATTGCCCTGAGTCTGCGCAGGAGGCACCTTGTCTGGCCAGAGAGAACTCATGGCCC	61346
QY	2424	-----	2423
Db	61347	CTGGCATGACTCTGAGTAGGTATTGAGGCTGCAGGGCCTTGGGCGTCCAGAGGCAGCTG	61406
QY	2424	-----	2423
Db	61407	GTATGCCCTCTGCACTTCAGCCCCATGGATGGATGATACAGGCCTGCTGTTCAGA	61466
QY	2424	-----	2423
Db	61467	AAGGTCAGAGCCTTTAGCAGGGAGGCAGCAGAGCTGGGCTAGACCTCAGGTCACTAAG	61526
QY	2424	-----	2423
Db	61527	TGAATCTGAGCAAGTCAGTGAACAGTCTCTTCTCTTCAATTTCTCCACCTGTAAGCCAGGT	61586
QY	2424	-----	2423
Db	61587	ATGATAAACGCCATACAGCGCTTAGTGACAAACACATAAACTGTAGCTCCTGCTCTGT	61646
QY	2424	-----	2423
Db	61647	AGCAGAGGTGACAGCCAAGGCGAGTCTGTGCTATCCAGGCCTGGTAGGGGGCAGCCCTC	61706
QY	2424	-----	2423
Db	61707	GCCTCAGTTGAGGGCTGAGGGAGAGACTGAGGTGCAGCAGATGGCAGTGGTAACCAAACC	61766
QY	2424	-----	2423
Db	61767	AGTTCCCTTGCCGTGGGTGGGACACAGAGAAAGCAGCAAGCAATCTGGAAGTGAAGT	61826
QY	2424	-----	2423
Db	61827	CAGGACAGGAGGCTCAAGCCTGGGTGAGTCAGGAGTCCGGGGCTTTCTTTTCAATCCAAC	61886
QY	2424	-----	2423
Db	61887	CCATTGCTGCTGCTCGGCAAAAGCCAGCCAGCCAGCCGCTGGCCCTTCCCGCTTCT	61946
QY	2424	-----	2423
Db	61947	TCAGACTCTAGGGTAGCCCGCCAGCGACACACAGAAACCAAGTGCACGGGGCGG	62006
QY	2424	-----	2423
Db	62007	GTGTCCTCCACGAGATTTCTCTCTGTGTCACATCTACGTAATTTTACTCTGTTTACAGTCAA	63146
QY	2424	-----	2423

Db	62067	CTCCTTGGACCATCAGCTTTACAGTCCAGACCACCTGCAGCCACCGGTGGTCTCCAG	62126
QY	2424	-----	2423
Db	62127	CTCCCCAGTCTCGGCAGGATGGCTTTTGAGCCTGTTGGAGAGACCTTTGCCAGGAGAA	62186
QY	2424	-----	2423
Db	62187	TGCTGCCCAGGGCAGCAAGACAGACTCTGGAGCTAGAAGAGTTGCCGCCCAGG	62246
QY	2424	-----	2423
Db	62247	GGCCAGGCCACTCCAGAGGACAGGAGGCCCAAAAGCGGGAAAGGCTCCATGTTACGG	62306
QY	2424	-----	2423
Db	62307	TGCCCCCATGCTGGGAGTTTGTCTGCCCTTCTCTCTCCCTGACTGCCAAGCGTGGGGTG	62366
QY	2424	-----	2423
Db	62367	GTCTGGGCAGGAGGCATCCTCTGGTGTTCCTTAGCAGCCCGCTGTGTGCAGGGGCTC	62426
QY	2424	-----	2423
Db	62427	CCATTTTGTCTCTAGCTGCAGAGGGCCACAAAGGAGGGGCTCATGGGACTGCTG	62486
QY	2424	-----	2423
Db	62487	AGAAAGGTGTGCAGAAAGGAGTGTGGCCCTAGATCAGTCTCTTTAAAAGCCTCTGTT	62546
QY	2424	-----	2423
Db	62547	ACCTGAAAGAGGTCAAGCAGAGAGAGGAATGGCTGCTGTGTCTACCGGGCAGGACAG	62606
QY	2424	-----	2423
Db	62607	GACAGAGGAGGTCAATTGTTACACACACATCCCCCTCTCTCTCTCCCTCCACCTT	62666
QY	2424	-----	2423
Db	62667	CCGTGTAAGCCTGAGGCAGGCTGTGGCCAGGCTCAGGCCCTGACTGTGGGGTACACAC	62726
QY	2424	-----	2423
Db	62727	CAGGAGGCCACGCCTCCCCACAGACGGGGTGGAGTGTGCTAGTGAGCCAGCACCCCTCT	62786
QY	2424	-----	2423
Db	62787	GCTGCTTCAGCATCTCCGCTGGAGCCAGCTGTCCCTCTCTCTCTCAGGCTCCATCCGAAC	62846
QY	2424	-----	2423
Db	62847	AAAAGGAGCAGAGCCTGAGATCCGGCACCCCATCCCCCTCCACTCAGCACTGAGTTAG	62906
QY	2424	-----	2423
Db	62907	AGCTGGTGGGGCATGTCTGCTTCACACGCTGCCTTATGGCTTCTGTCTCTCCAACAG	62966
QY	2424	-----	2423
Db	62967	CCCTCAGCCTCTGGCTGCTCTCTTCCCAATAGTCACAAGATTTACCATGATAATAATAG	63026
QY	2424	-----	2423
Db	63027	GTTAAGACTTGAATGGTGTGTTTTTCACTCTTCACTCTCCCTGTCTCAGCTTACGTTA	63086
QY	2424	-----	2423
Db	63087	TTTTTATCCTGATGACAGAATAGGTACTACAGTATTTTACTCTGTTTACAGTCAAA	63146
QY	2424	-----	2423

Db	63147	GAACCTGAGGCACAGGCAGGTTTGCCCAAGGTCACATAACTGCTTAATAGCAGGGTAGAC	63206
QY	2424	-----	2423
Db	63207	AGGTGAAGTAACGTGATGTATCAGCCATGCCCTTTCCCATGCCCCGGGCACTCCCA	63266
QY	2424	-----	2423
Db	63267	TGACAGCTCTCTGAATCCCAACATTTATTTCTTTGCAGGATTAGACCAAGCATATAA	63326
QY	2424	-----	2423
Db	63327	TTCCCTTTTCCCTCTCTCCATCCACATTCCTTTATTTTACGTACTACTATAGGCCT	63386
QY	2424	-----	2423
Db	63387	TGTAGGGCTCTGTCAACAGACAAAGGCCAGGTCGTGGCTGATGCCGTGAATCCCA	63446
QY	2424	-----	2423
Db	63447	TGCTTTGGAGGCTAGGCATTTGAGACCAACCTGGGTAAACAAAGCAAGACCGGTCCTA	63506
QY	2424	-----	2423
Db	63507	TAAAAATAAAAATTAACCCGGGTATGGTGTGCACCTGTAGTCTAGCTACTTGGGAG	63566
QY	2424	-----	2423
Db	63567	GTTGAAGTGGGGGATCACTTGAGCCCAGGAGTTCGAGGTTACAGTGAGCTATAACTGA	63626
QY	2424	-----	2423
Db	63627	CTCGTCTTCTTTGGTTGACAGAGAAAGACTCTGCTCTAAAGAAAAAACCAAGAC	63686
QY	2424	-----	2423
Db	63687	TGGTAGTTCTGGCCCTCATGGGGTCAATCATCCAGTAGGCAGCAAGACTATCAGTAAC	63746
QY	2424	-----	2423
Db	63747	AAAGATGCCGAGGGATAAAGTCCAGAGCAGCAGAGAAATCCAGGGCTGCAGATCTCAGTG	63806
QY	2424	-----	2423
Db	63807	CTTACCCCAAGCATTAAGCCCCAGAGCTGCTCCCGTTGGAGCATAGGTTTCATAGCCCCAG	63866
QY	2424	-----	2423
Db	63867	CTCCCTGAGCCCTGCACAGCTCTGTCCCTGAGATGGGATGCTCTCCACTCATCACTG	63926
QY	2424	-----	2423
Db	63927	GCACAAGCCACCTGAGTAGCAGGCAGGATATGTGGCTGGTGGCTGCAGCAAAATCTGACC	63986
QY	2424	-----	2423
Db	63987	TGGCAGTTGCTCAACCCCTTCTCCCTTCCACAGACCTACAGCCCAAGAGTACATGT	64046
QY	2424	-----	2423
Db	64047	CTTTCCAAAATGTCTTAGTACCCCAACCCACACTCAGATTGAGCTCCTCCTACATCT	64106
QY	2424	-----	2423
Db	64107	GCCAGGCCATGGATCTATACTAAGTAAGTGTCCACCCAGGCCTGTCCAGTTGCTGCAGCC	64166
QY	2424	-----	2423
Db	64167	AAATTCAGCACCCTCTCTCAGATTCTGGACTCTTCAAGACCTGAGCTGTAGCCTTCCTG	64226
QY	2424	-----	2423
Db	64227	CAACACGTCTGCTGGCATCTGAGGGTGAAGGGCTTGACAGCCAGGCGACGGGTGACTG	64286

QY	2424	-----	2423
Db	64287	CCGTCCCTCCAGTCATGATAAACTGGATCATCTCTGAGAAGCCAGTCTGACTCAGCTG	64346
QY	2424	-----	2423
Db	64347	CACTTAGAAAGAGTCTTCTCTCCCATGCTTGGGGCCTTCTCTGGAGCAGGTGCTCGATG	64406
QY	2424	-----	2423
Db	64407	GGGTCAAGGGAGGATGCTCCTGGTGGTAGCTAGCTAGAAACACAGAGAGGCTGGTACTCC	64466
QY	2424	-----	2423
Db	64467	CAGAAGAAGACAGAAGGTTAAGCTCACAGTTTGGACCCACTTTTGTGCTAGGAGGTGTG	64526
QY	2424	-----	2423
Db	64527	GGATTCTGGTTGTGCATGTGTGTGGACTGTGACCAAGTGTGCACCCTGGACCAGGAGC	64586
QY	2424	-----	2423
Db	64587	TGGATGCTCAGGCTTCACCCTGACTCTGCCCTTGCTCTTGGCCCTTGGAGAGCACT	64646
QY	2424	-----	2423
Db	64647	TGGATCTTTGGTTTCTCACTGGAGTGAGTTGTAGGCAGCTAGAGCTGTTTGGACTGCTG	64706
QY	2424	-----	2423
Db	64707	AATGAGGGGCTGTACTTGGCTTCTCGCACTTAGCGCATCTAGCTAGCAGAGGGTAG	64766
QY	2424	-----	2423
Db	64767	AGACAGGTGCTTTTATAGGGGGCCATGACAACAGGATATTTAAGCTTACTTGACCACC	64826
QY	2424	-----	2423
Db	64827	CAGAAAAGTGCCTCTCCACCAGAGTATAAGGCAGCATAGGTGGATGCCATAGTTGGCA	64886
QY	2424	-----	2423
Db	64887	GTGTCTGGGCGAGGGGGCTCCATCTCTCAGAGCCCTGGGCAAGCAAGCGCTTCC	64946
QY	2424	-----	2423
Db	64947	TCTCCCTGGGCTCACTTTCCCATTTAGAAACAGGAATTTGGATGAGAAGTGTGTGAGG	65006
QY	2424	-----	2423
Db	65007	ATCTATGAATTTGGCAACTCAGGGTGTCAAAAGGGGAAGGGGTGTAGGCCCTTTAAGCA	65066
QY	2424	-----	2423
Db	65067	TCTTCCCATGCTGCTTCCAGCCGTGACTGCTCATGGAGGATAGTGAGCTGCAAGCA	65126
QY	2424	-----	2423
Db	65127	CTGTTTTATGGAGGGTTCTCAGAGCTCCCTACCCCTGAGTGTGCTCCTGCTACCTG	65186
QY	2424	-----	2423
Db	65187	CTTGAGTGCATGACTGCTTGCCTTCTACTCTTTGAGTTCTAGTTGTCAGTAGAAGGCCCC	65246
QY	2424	-----	2423
Db	65247	TGTTATGTAGATACATAAGTTGGGAAGATTCTTAATGGCCCAATTGTAGATTCTAATTAAT	65306
QY	2424	-----	2423
Db	65307	ATTTCTAATGCTCACTTTTAAAGAAATAGAAAAAGAGAGCCTCGAGGCAATGGCATTAG	65366

Qy	2424	-----	2423
Db	65367	GGGAATTTAATGCGATGATCAGGTGGCAAGTCCAGAGATGAUTTACTTTAGGTGGGAGAA	65426
Qy	2424	-----	2423
Db	65427	TGTTACAGGGTCTCTGGGACACAGGGCATCCAGGGTGGGAATCAGAGGGAGAGTAGGTG	65486
Qy	2424	-----	2423
Db	65487	GCCAGTTTACCCCTCTCAGCGTTGCTGGGGCTGAGCCCTGCAGGCAACCTGTGTGCTG	65546
Qy	2424	-----	2423
Db	65547	GAGGAGAGCCTGCACATGCAGGCTGGACTCTGGTGGCCACGGAAGTGCAGCAATCT	65606
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DEFINITION Homo sapiens, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.
ACCESSION AC004241
VERSION AC004241 GI:3046263
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158766)
Muzny D., Aronson, A.D., Brundage, E., Carvelli, K., Chen, E., Di, W.,
Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C.,
Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L., Kampal, R.,
Karpathy, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., Ly, T.,
Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Rowland, K.,
Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J., Vo, Q.,
Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 158766)
Worley, K.C.
Direct Submission
Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[WARNING] On May 2, 1998 this sequence was replaced by a new
version gi:3108007.
On Apr 13, 1998 this sequence version replaced gi:3023023.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 72370: contig of 72370 bp in length
* 72371 72390: gap of unknown length
* 72391 113183: contig of 40793 bp in length
* 113184 113203: gap of unknown length
* 113204 153083: contig of 39880 bp in length
* 153084 153103: gap of unknown length
* 153104 154799: contig of 1696 bp in length
* 154800 154819: gap of unknown length
* 154820 155804: contig of 985 bp in length
* 155805 155824: gap of unknown length
* 155825 156627: contig of 803 bp in length
* 156628 156647: gap of unknown length
* 156648 157381: contig of 734 bp in length
* 157382 157401: gap of unknown length
* 157402 158103: contig of 702 bp in length
* 158104 158123: gap of unknown length
* 158124 158766: contig of 643 bp in length.
Location/Qualifiers
1..158766
/organism="Homo sapiens"
/mol_type="genomic DNA"

FEATURES
source

BASE COUNT 46074 a 35904 c 34654 g 41968 t 166 others
Query Match 95.0%; Score 2312.4; DB 10; Length 158766;
Best Local Similarity 16.2%; Pred. No. 4.5e-126;
Matches 2433; Conservative 0; Mismatches 1; Indels 12584; Gaps 12;
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Db 72996 CAAGGATCCGATGGGTATATGGAGTGTGAGGTAAATGGATCATTTATGTTGGAAGGATGAG 73055
Qy 61 GGGGTTTTTGTAGACACAGGTTTGGAAAGAGAGTTTACGACACTGCTGCTAGTTTGGGAATCA 120
Db 73056 GGGGTTTTTGTAGACACAGGTTTGGAAAGAGAGTTTACGACACTGCTGCTAGTTTGGGAATCA 73115
Qy 121 CCCATGTCGAGCGGCACATGAGGCAGTAAAGAACTCTGCAGGGGTCCCTGAGATTTTGA 180
Db 73116 CCCATGTCGAGCGGCACATGAGGCAGTAAAGAACTCTGCAGGGGTCCCTGAGATTTTGA 73175
Qy 181 AATGTAGGAAGAGCAATGGATTGAGTCCGAACCTGGAGGATCTGCTATACGCAAGCT 240
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Qy 241 GGGAGGAGGACAGAGTCACTACAGAGTCCGAAAAAGAGGAGGTTGGAAAGGGAACCTG 300
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Db	74256	GCCTCTCCCTCCTGGGTGGAGATCAGGCAGCCCTTCCACAGCTCAGTCTGGTCTCCT	74315	Qy	1163	-----	1162
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D	b	79176	TTCACTTTTCTGGGCTACAGGAGGCAGAAGTTTGGGACCTATGAACAAAACCCATCT	79235	
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D	b	79296	CTTTGAGAAGATGGTGAGTCCAGGGAGAGCAGGCATTCACTACTAATATAGTTGGAGGA	79355	
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QY	2424	-----	2423
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Db	84936	TGGATCTTGGTTTCTCACTGGAGTGTGTGAGCAGCTAGAGCTGTTTGGAGCTGTG	84995
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Db	84996	AATGAGGGGCTGTACTGGCTTTCCTGSCACTTAGCGCATCCTAGTAGCAGAGGGTAG	85055
QY	2424	-----	2423
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QY	2424	-----	2423
Db	85116	CAGAAAGTGGCCCTGCCACAGAGTATAAGSCAGCATAGTGGATCCCATAGTGGCA	85175
QY	2424	-----	2423
Db	85176	GTGTCTGGGCGAGGGGGCCTCCATCTCTCAGCAGCCCTGGGCAAGGCAAGCGCCTCC	85235
QY	2424	-----	2423
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QY	2424	-----	2423
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RESULT 7
AC004241
LOCUS Homo sapiens, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.
DEFINITION AC004241
ACCESSION AC004241
VERSION HTG; HTGS_PHASE1.
KEYWORDS HTG; Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

REFERENCE
AUTHORS

Primates: Catarrhini; Homnidae; Homo.
1 (bases 1 to 158784)
Muzny, D., Arenson, A.D., Brundage, E., Carvelli, K., Chen, E., Di, W.,
Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C.,
Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L., Kampal, R.,
Karpathy, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., Ly, T.,
Martinez, C., Osval, G., Perez, L., Rashid, N.D., Rowland, K.,
Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J., Vo, O.,
Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 158784)
Worley, K.C.
Direct Submission

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[WARNING] On Jul 1, 1998 this sequence was replaced by a newer
version gi:3282154.

COMMENT

On May 2, 1998 this sequence version replaced gi:3046263.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

- * 1 72370: contig of 72370 bp in length
- * 72371 72390: gap of unknown length
- * 72391 113202: contig of 40812 bp in length
- * 113203 113222: gap of unknown length
- * 113223 153101: contig of 39879 bp in length
- * 153102 153121: gap of unknown length
- * 153122 154817: contig of 1696 bp in length
- * 154818 154837: gap of unknown length
- * 154838 155822: contig of 985 bp in length
- * 155823 155843: gap of unknown length
- * 155844 156645: contig of 803 bp in length
- * 156646 156665: gap of unknown length
- * 156666 157399: contig of 734 bp in length
- * 157400 157419: gap of unknown length
- * 157420 158121: contig of 702 bp in length
- * 158122 158141: gap of unknown length
- * 158142 158784: contig of 643 bp in length.

FEATURES
source
1..158784
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 46083 a 35920 c 34642 g 41973 t 166 others

Query, Match 95.0%; Score 2312.4; DB 1; Length 158784;
Best Local Similarity 16.2%; Pred. No. 4.5e-126;
Matches 2433; Conservative 0; Mismatches 1; Indels 12584; Gaps 12;

QY 1 CAAGATCCGATGGGTATATGGAGTGTAGGTAATGATCATTCATGTAAGGATGCGAG 60
Db 73015 CAAGATCCGATGGGTATATGGAGTGTAGGTAATGATCATTCATGTAAGGATGCGAG 73074
QY 61 GGGGTTTTGAGACCCAGGGTTTGGAGAGAGTTTCCAGTCTGCTGGTAGTTTGGGAATCA 120
Db 73075 GGGGTTTTGAGACCCAGGGTTTGGAGAGAGTTTCCAGTCTGCTGGTAGTTTGGGAATCA 73134
QY 121 CCCATGTGAGCGGCACACATGAGGCAGTAAAGAACTCTCAGGGTCCCTGACATTTGGA 180
Db 73135 CCCATGTGAGCGGCACACATGAGGCAGTAAAGAACTCTCAGGGTCCCTGAGATTGGA 73194
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Db 73195 AATGTAGGAAGAGCAATGATTTGAGTCCGACCTGGAGGATCTCTATACGACAGCT 73254
QY 241 GGGAGAGGACAGAGTCACTACAGTCCGAAAGAGAGGTTGGGAGGGAACCTG 300
|||||

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Db	76435	GATGCCCGTGTGTGGCCACATCTCTGGGGCTCAATGAGCGTCTCTTTGTTGTCAACCCA	76494
QY	1244	CAGGAAGTGCATGAGCT	1260
Db	76495	CAGGAAGTGCATGAGCT	76554
QY	1261	-----	1260

Db	76555	TTTTGAGTGTGGCAGTGGTGGATTCTGGGGAGGTTCCAGGAGAAAGGAGGAGGGGC	76614
QY	1261	-----	1260
Db	76615	CTGGCTCTGGCTGCTGCTGGTCTCTCAGCACACAAAGGAGTGGGCCCTCAGCTCATGGGG	76674
QY	1261	-----	1260
Db	76675	AATTTCCAAAGATAGTGCAGGGCAGGGCTGGTAGCACTGGTTGGAGCTCCCAAGAGAA	76734
QY	1261	-----	1260
Db	76735	AGAGGAGACCTGCCCTAGTTAGGGTTCCCCAGAGACAGAGAGAGAGAGGGGTC	76794
QY	1261	-----	1260
Db	76795	TCAGCACTGGGGAGCCCTATCTCCAGCTGCTATAGCCCCCTAGAGACCCTCTACTCCCCA	76854
QY	1261	-----	1260
Db	76855	CTCTGCCCTCCTAAACCTCCTCTTAACACAGCATAGAGTCTTGGCCCCAACCTCTCC	76914
QY	1261	-----	1260
Db	76915	CCCTACCCTGTGCTTTTCCCTTGGATTCTCAGCAGCCCCCTGAGCACTCTCCCACCCG	76974
QY	1261	-GATCCACACACCTGACAGCTGGGCCCTCTGGCTCTGCTGAGGGCTGAGCTGG	1319
Db	76975	AGATCCACACCTGACAGCTGGGCCCTCTGCTGAGGGCTGAGCTGG	77034
QY	1320	TGAGTCCCAAGGACCTGGCAGGCTGACGACCAACGACACTGGAGCTCTTCAACAGTA	1379
Db	77035	TGAGTCCCAAGGACCTGGCAGGCTGACGACCAACGACACTGGAGCTCTTCAACAGTA	77094
QY	1380	TCCA-----	1383
Db	77095	TCACACAGGTATGGGAGCAGAGCTGGGGAGGAGAGCAGCGCGGGCGCCGCTCG	77154
QY	1384	-----	1408
Db	77155	GCTCAGCACTCGCTGACCTCTCTCTGTGACCCCAACCCAGGTGGAGCTGATCCACTATGTG	77214
QY	1409	CTGGGCCCCAGCATCTGGGGATGTCACCAACGCCAACCTGGAGGCTTTCATGCGCCG	1468
Db	77215	CTGGGCCCCAGCATCTGGGGATGTCACCAACGCCAACCTGGAGGCTTTCATGCGCCG	77274
QY	1469	TTCAATGAGCTGCAGTACTGGGTGGCCACCGAGCTGTGTCTGTGCCCCGTGCCCGCCCC	1528
Db	77275	TTCAATGAGCTGCAGTACTGGGTGGCCACCGAGCTGTGTCTGTGCCCCGTGCCCGCCCC	77334
QY	1529	CGGGCCCACTGCTCAGGAAGTTCAATTAAGCTGGCGGCCA-----	1569
Db	77335	CGGGCCCACTGCTCAGGAAGTTCAATTAAGCTGGCGGCCCACTGTGCTGCCAGTGG	77394
QY	1570	-----	1569
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QY	1570	-----	1569
Db	77455	TGTTGCCAAATCTGCCACCTATTGTTCCCTGGGTCCCTGGAGCTCTGCTTCCCCAC	77514
QY	1570	-----	1569
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QY	1570	-----	1582
Db	77575	GTGGCTGCTTCCCTTACCCTGAGGGTCTCTGGGTCTTCTGCTCACAGCTCAAGAGCAG	77634
QY	1583	AGAAATCTCAATCTCTTTTGGCGTCAATGTTGGCTCAGCAACTCGGCCATCAGCCG	1642

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QY 1643 CTAGCCACACCTGGG----- 1658
Db 77695 CTAGCCACACCTGGGAGGTAAAGTGTGCTGGAGGGCCCTCTCTGAGGTCAGGCCCTCA 77754
QY 1659 ----- 1658
Db 77755 GGCCTCTCTGGAGTGTGGATGGGGCTGGGCCTCCCCCAGAGAGCCGCTCATCTGCCT 77814
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QY 1760 TCCCTCTCTGTATCCCTTTCATGCCCCTTCTTCTCAA----- 1797
Db 78835 TCCCTCTCTGTATCCCTTTCATGCCCCTTCTTCTCAAAGGTAAACAGGGCTTCTCGCTC 78894
QY 1798 ----- 1797
Db 78895 CATCCTCAATTCCCCCTTCTCTGCTCCATCCCAATTTCCCTTCTCTGCTCCATCC 78954
QY 1798 ----- 1797
Db 78955 CCCATCCCATGCCCTATCTGTGTGTCACCCACTCTGTTTGGAGAGATTTATACCTCAAGTGC 79014
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Db 79015 TGATGCCCTCAGGAGTGCAGAGATCAATTAGGAGTTCTTAGACTTGAAGAATGAAGACAT 79074
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QY 1798 ----- 1797
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Db 79255 CTTTGCACATACCTTTCATTCATGAGGAAACACACACTAGTGGAGAATCTCATCAA 79314
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Db 79315 CTTTGCAGAGATGGTGTAGTCCAGGAGAGCAGGCAATTCACACTACTAATAGTTGGAGGA 79374
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Db 79795 TGCTGCACCACTGCGGAAGCCACAACTCTGCTGAGAGGGGCTCCCGGGGTGGAGGT 79854

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Db	80035	CTTATGCTAGTTACCCATGSGTGGCACATCCTAGGCACCTTGCCATGTGCCAGGCAGGAG	80094
QY	1992	-----	1991
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QY	1992	-----	1991
Db	80155	TCCTTCGTCCTCCCTCACCCTGGGGTGGGCGAGGACAGCCCTCTTTAGGAATGGTGATGG	80214
QY	1992	-----	1991
Db	80215	GAAGTGGTTGGTGGTGGAGGGCAAGAAGGCAGATGTATGGCTCTTGGAGGGG	80274
QY	1992	-----GCT	1994
Db	80275	AAAGTTGGGTTCCACAAGGGGCATCAGTGCCTCCTGACTCTCCTCCACCAGGCT	80334
QY	1995	CGGAGCAGTCCCTGAGCACCCGAGTCCAGCCAGCACCTGGGCTTATGTCCACGACTGA	2054
Db	80335	CGGAGCAGTCCCTGAGCACCCGAGTCCAGCCAGCACCTGGGCTTATGTCCACGACTGA	80394
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Db	80455	GGGCTGGGACTGGAGCTGGAGCAGGCACTTGCAGCCGGAAAGCCAGGGTGTCCGGGCC	80514
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Db	80515	AGATATCTCACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGTGGAGTGGACTCGAGTCCC	80574
QY	2235	TGGAGCAGCAGTGTGGAGGACCCATCCCTGTGTATGACTGGCAGCTAAGGAGGACCTC	2294
Db	80575	TGGAGCAGCAGTGTGGAGGACCCATCCCTGTGTATGACTGGCAGCTAAGGAGGACCTC	80634
QY	2295	GGAGTGGACCCGAGCCAGGAATAACGAATGACCCAGGCCAAGGAGGAGGACAGAGAG	2354
Db	80635	GGAGTGGACCCGAGCCAGGAATAACGAATGACCCAGGCCAAGGAGGAGGACAGAGAG	80694
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Db	80695	GGCCCAAGGAGTGGGTGGAGTGGAGTGGCGCTGGGACGTTGTGTGCAATAGAGAGTCTC	80754
QY	2415	CACACCAGA	-----
Db	80755	CACACCAGATGTCTTCCAGATTCTGTGCTCTGGCTTTGTGTCTCCAGCCAGGCTGCAGT	80814
QY	2424	-----	2423
Db	80815	TTATTTTCACAGTGGACAGAGAGAGAGAGGCTGCAATGTGTACCGTGTGGCAA	80874
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Db	80875	GGCAGGGCTTGGCTGGGCGAGGGCCCCCTGCTTTCTTCCACAGCTTTCTTCCAAAC	80934
QY	2424	-----	2423

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Db	80995	AACATAGTAGTATGTTTCCAGGCCACCCAGAGTGGGGTGGCAGGAGGCTGAGGCCCG	81054
QY	2424	-----	2423
Db	81055	CCCTCTGGGAAGGAGCTGTGGAGGAGAAGCAGCCCCATGCTGGGCACGGGCCAGACTGGG	81114
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	81415	TTCCAGGAATCAGGGTTTATCATCAGTGTGAGATGTTCCAGCAAGCTCTGGTCATA	81474
QY	2424	-----	2423
Db	81475	CGAAGTCTCTCTTCCCTGCCCTTCCAGCAGCTTCCCTTAGGAACAGTACTGCCAGGAC	81534
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Db	81655	CTGGCATGACTCTCTGAGTAGGTAATTGAGGCTGCAGGGCCTTGGCGTCCAGAGCAGCTG	81714
QY	2424	-----	2423
Db	81715	GTATGGCCCTCTGCACCTTCAGCCCCATGGATGTGGATACACAGGCCCTCTGCTTCCAGA	81774
QY	2424	-----	2423
Db	81775	AAGGCTCAGAGCCTTTAGCAGGGAGGCACACAGCTGGGCTTAGACCTCAGGTCACATAAG	81834
QY	2424	-----	2423
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RESULT 8

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AC004241
LOCUS
DEFINITION Homo sapiens, 155147 bp DNA linear HTG 14-MAR-1998
ACCESSION AC004241
VERSION AC004241 GI:2960506
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS Muzny,D., Aronson,A.D., Brundage,E., Carvelli,K., Chen,E., Di,W.,
Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesha,R., Garcia,C.,
Goodman,M., Gorrell,J.H., Haywood,M., Jackson,L., Kampal,R.,
Karpathy,S., Leal,B., Li,Y., Liu,W., Logan,O., Lu,J., Ly,T.,
Martinez,C., Oswal,G., Perez,L., Rashid,N.D., Rowland,K.,
Savage,L., Scherer,S., Shen,H., Timms,K.M., Todd,J., Vo,Q.,
Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.
1 (bases 1 to 155147)
2 (bases 1 to 155147)
Direct Submission
Unpublished
Worley,K.C.
Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
[WARNING] On Mar 21, 1998 this sequence was replaced by a newer
version gi:2980958.
On Mar 14, 1998 this sequence version replaced gi:2943840.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Db	1648	GTCACTTTTCTGGTCTTCTCAGTGTGAATGATGCTAGCATTAATGGAGGTGGAGTGC	1707
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Qy	1163	-----	1162
Db	1828	CTCTGCTCAGTTTTTATCATCCATAAAATGGGAATAGTAGGAGTACTTGCCCTCGGAG	1887
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Db	1948	GTGATACATAAGTATTAGTCTGCTATTATTATCATCATTTGTGTTTAGTCATTTAATATGA	2007
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Db	2008	ATTAATAACAATCTCATGAGATACAGTACTTTTATCCTATTTCAGACAAGAACACTGA	2067
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Db	2248	GAGCATAGAGGTGGACTCCAGACCCGTTGAGGCATCTTAGGCTCACCATTTACTAGCT	2307
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Db	2308	GTGTGATGTGGGCAAGTTGCTTAACCTCTCTGAGCCTGCATTTCTCACCTGTGCAGATG	2367
Qy	1163	-----	1162
Db	2368	AGGACTGTAATTGTATCTACCCACAGGGTTGCAATGGCTAAGTAGCTAAATGTGTATAA	2427
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Db	2428	GCACTTAGCACAGGGCCTGCCAGTCAGTCTGAGAACATGGCGGCTCAGGAGTATTAA	2487
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Db	2488	ATGGGCCCTCCAGAGAACCTGGAACATTCAAAACCACCTGTCTCTCGGGAGGCCACGGCT	2547
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Db	2548	TCAGACTGGAACCCAGGCAGACAAGAAATTAGGGCGTTCAAGAAAGTGGGATGAGAAA	2607
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Db	2608	AGAAAAGCTTCTCCCTTCAGGAAGTGGGGAGAGATGGTCACCTGTGTGCCCTGCCCTGG	2667
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Db	2668	GAAGCACTGCCCTCTGCTGGCCACCTGGTGTGAGTTGCAGTTGCCAAAGGTCTGTTATT	2727
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Db	2728	GAGACCTTACTATGTGCCAGGCACCTGTTTAGAGCACTGATCTCCGAAGCACTTGGATCGA	2787
Qy	1163	-----	1162
Db	2788	CACCCATGTCAATAACCAACATTTAAATTAAACCACACCCACACTGTGTGAATATTGTT	2847
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Qy	1163	-----	1162
Db	3268	TCATGAGAACTTTTCTCATCTCTTGATGTGCTTCCCTGGGCTGGCTGGCTGGCTGGCTGG	3327
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Db	3328	GCACATGCACCTGTGTATTCTCAGCACCAACCCAGGACTTCAACCCCGCTACTAGGAGAAA	3387
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Db	3388	CAACCTCTCAGCTCCCAAAACAGCACCTCCACCTTGGCATCCAGCTGGTCCCGGCCCTCC	3447
Qy	1163	-----	1183
Db	3448	CTCCCTTCTGACACAGTCCGCTCTGCTGCTTTTGCAGATGCCATTTGGCTGCAGCCA	3507
Qy	1184	GATGCCCTGTGGTGGCCACATCTCTGGGCTCAATGAGCGTCTCTTTGTTGTTCAACCCA	1243
Db	3508	GATGCCCTGTGGTGGG-CACATCTCTGGGCTCAATGAGCGTCTCTTTGTTGTTCAACCCA	3566
Qy	1244	CAGGAAGTGCATGAGCT-----	1260
Db	3567	CAGGAAGTGCATGAGCTGGTAGGACAGGAGGTGCCAGGCCAGGAGGAGGAGATCTA	3626
Qy	1261	-----	1260
Db	3627	TTTTGAGTGTGGCAGTGGTGGATTTCTGGGAGGGTCCAGGAGGAAGAGGAGGAGGGC	3686
Qy	1261	-----	1260
Db	3687	CTGGCTTGGCTGCTGGTCTCAGCACACAAGGAGTGGGCTCAGCTGATGGGGG	3746
Qy	1261	-----	1260
Db	3747	AATCCCAAGATAGTGCAGGCGGGCTGGTAGCACTGGTTGGGAGCTCCCAAGAGAGAA	3806
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Qy	1261	-----	1260
Db	3927	CTCCTGCCCTCCTAACCTCCTCCTTAACAGAGATAGATCCTTGCCCAACCTCTCC	3986
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Db	4287	CTGGGCCCCAGCATCTGGGGGATGTCACCACCGCAACCTGGAGCGCTTCATGCGCCGC	4346
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Db	4347	TTCAATGAGTGCAGTACTGGGTGGCCACCGAGCTGTCTCTGCCCGCTGCCCGGCC	4406
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Qy	1570	-----	1569
Db	4467	GTAGGGGTGGCCAGAGTCCCCCGGTACCTTTTCTTAAGCCCCCTCTTTGCTAGTA	4526
Qy	1570	-----	1569
Db	4527	TGTTGCAATCTGCCACCCTATTGTTCCTGGGTCCTCGAGGCTCTGCCTTCCAC	4586
Qy	1570	-----	1569
Db	4587	CCATCCAGCTGGATCTCTGCAGAGGCTGGCCTGGCTGTGTCTGGGGSCACTGTAGGG	4646
Qy	1570	-----	1582
Db	4647	GTGGCTGCTTCCCTTACCCTGAGGTCCTGGGTCTCTGTCTCAGAGCCTCAAGGAGCAG	4706
Qy	1583	AGAAATCTCAATTCCTTTGCCGTCATGTTTGGCTCAGCAACTCGGCCATCAGCCGC	1642
Db	4707	AGAAATCTCAATTCCTTTGCCGTCATGTTTGGCTCAGCAACTCGGCCATCAGCCGC	4766
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Db	4767	CTAGCCCAACCTGGGAGTAAGTGTGTGTGGAGGGCCCCCTCTCTGAGGTCAGGCCCTCA	4826
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Db	4827	GGCCCTCTTGGAGTCTGTGATGGGCTGGGCTCCCCCAGAGCAGCCGCTCATCTGCCT	4886
Qy	1659	-----	1709
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Db	5067	CAGGGTTCCCAACCTCGGCCACGGGCTAGCTCCAGCTGTGAGTTTGGGAGCTGGCTG	5126
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Qy	1711	-----	1710
Db	5247	GGGTCTGAGTGGCCAGGGCAGTGTCAAGGGGCTCCAGAGCCCAAGGGCTTGGCATGGAGCG	5306
Qy	1711	-----	1710
Db	5307	CCTGTGTGCACAGGGCTGTCTGCCCTCAGGAATCCGAGGGGCTTGGGGCTAGACC	5366
Qy	1711	-----	1710
Db	5367	AGTAGAGAGCGGAGGATAGAGTTGGGGGTGGAACCTCCACCTCCAGGAACCTTTTGAGG	5426
Qy	1711	-----	1710
Db	5427	ATTTTGGGGTTTTGACTATTCTGGAGAGAAGCAGAGAGTACTTTCATCAGCATAGC	5486
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Db	5487	CTGGAGCTCTTGAGAGAAATCCACCTCTGGGGCTCAAGGGATTCAAAGGAGTTTACT	5546
Qy	1711	-----	1710
Db	5547	CTCAGAGAGAGAGAGGGGACACAGAAAGACAGAGGATAGAAAGGACAGAGAGT	5606
Qy	1711	-----	1710
Db	5607	GACAGTGACAGACTTTTCCAAGAAACCTGGGGCCCTGTGACTTAAGTGTGCTGAATTTTC	5666
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Qy	1798	-----	1797
Db	5967	CATCCCTCCATTCCCCCTTCTCTGCCTCCATCCCCCATTTCCCCCTTCTCTGCCTCCATCC	6026
Qy	1798	-----	1797

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QY	2424	-----	2423
Db	8307	TAGGACTTTACAGTCCAGATGCAACTGACAGCTTCTTCCCAACTGCAATCCCCCGCTTTTC	8366
QY	2424	-----	2423
Db	8367	CACACTTGAGCTCGTCCCTGCTGTTGGGCCAGGCTTCTGGGGTCTTCTGGGGTGCGCTT	8426
QY	2424	-----	2423
Db	8427	GTGATAGAAACAATGCTGAAGCTTCCGCGGAGAGCCGCTGCTTGTGTTAGGGCCCAACAGA	8486
QY	2424	-----	2423
Db	8487	CTTCCAGGAATCAGGGTTTATCATCAGTGTGAGAAATGTTCCAGCAAGCTCTGTGTCAT	8546
QY	2424	-----	2423
Db	8547	ACGAAGTCTCTCTTCCCTGCCCTTCAGCACATTCCCTTAGGAACACGACTACTGCCAGGA	8606
QY	2424	-----	2423
Db	8607	CGCCTCTTGGAGGACAGAGCTCACCCAGGAAGCTCCAGGGACTCCACCCCTCTTGCCCTTGC	8666
QY	2424	-----	2423
Db	8667	TAATTGCCCTGAGTCTGGCAGCAGGAGGCATTTGTGTGCCAGAGAGAACTCATGGCC	8726
QY	2424	-----	2423
Db	8727	CCTGGCATGACTCCTGAGTAGGTATTGAGGCTGCAGGGCCTTGGGCTCCAGAGGCAGCT	8786
QY	2424	-----	2423
Db	8787	GGTATGGCCCTCTGCACCTTTCAGCCCCCATGGATGTGGATACACAGGCTGCTGTTCAG	8846
QY	2424	-----	2423
Db	8847	AAAGGTCAGAGCCTTTAGCAGGGAGGCACACAGCTGGGCTTAGACCTCAGGTCATAA	8906
QY	2424	-----	2423
Db	8907	GTGAATCTGAGCAAGTCAGTGAACAGTTCTTCTTCCCTTCATTCTCCACCTGTAAAGCAGG	8966
QY	2424	-----	2423
Db	8967	TATGATAAGCCCATACAGCGCTTAGTGACAAAACATAAACTGTAGCTCCTGCCCTCTG	9026
QY	2424	-----	2423
Db	9027	TAGCAGAGGTACAGCCAGGGCAGTCTGTGTATCCAGGCTTGGTAGGGGGCAGCCT	9086
QY	2424	-----	2423
Db	9087	CGCCTCAGTTGAGGGCTGAGGAGAGACTGAGGTGCAGCAGATGGCAGTGGTAACCAAC	9146
QY	2424	-----	2423
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QY	2424	-----	2423
Db	9267	CCCATTTGCTGTGGTGTCTCGGCAAAAGCCAGCCAGCCGCTGGCCCTTCACCGTTC	9326
QY	2424	-----	2423

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Db	9507	GCTGCCCAGTCTCGGCAGGATGGCTTTTGAGCTGTGTGGAGAGACCTTGCCAGGAGA	9566
QY	2424	-----	2423
Db	9567	ATGGTGCCAGGCGCAAGAGAGACACAGACTCTGGGAGCTAGAAGAGTTGCGGCCAG	9626
QY	2424	-----	2423
Db	9627	GGGCCAGGCCACTCCAGAGGACAGGAGGCCCAAGCGGGGAAGGCTCCATGTTACG	9686
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Db	9687	GTGGCCCATGCTGGGAGTTTGTGCTGCTTCTCCTGACTGCCCAAGCGTGGGT	9746
QY	2424	-----	2423
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Db	9867	GAGAAGAAGGTGTGAGAAAGGAGTGTGGCCCTAGATCAGTCTTTTAAAAAGCCTCTGT	9926
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	10347	GCCTCAGCCTCTGGCTGTCTCTTCCCAATAGTCACAAGATTTACCATGATAATAA	10406
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Db	10467	ATTTTATCCTGATGACAGATAGTACTACAGGTATTTTACTCTGGTTTACAGTCAA	10526
QY	2424	-----	2423
Db	10527	AGAACTGAGCAGCAGGAGGTTCGCCAAGTCAATAACTGCTTAATAGCAGGTAGA	10586
QY	2424	-----	2423
Db	10587	CAGGTGAAGTAACGTGGATGTGTATCAGCCATGCCCTTTCCCATGCCCCCGCACTCCCC	10646
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	11187	GCTTACCCCAAGCATTAAGGCCCAGAGCTGCTCCCGTTGGAGCATAGGTTTATAGCCCCA	11246
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Db	11307	GGCACAGCCACCTGAGTAGCAGGAGGTATGGTGGTGGTGGTGCAGCAAAATTCAGAC	11366
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QY	2424	-----	2423
Db	11427	TCCTTCCAAATGTCTCTAGTACCCCAACCCACACTCAGTATTGAGCTCCTCCTACATC	11486
QY	2424	-----	2423
Db	11487	TGCCAGGCCATGGATCTATACTAAGTGTGCCACCCAGGCCGTCTCCAGTTGCTGCAGC	11546

QY	2424	-----	2423
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QY	2424	-----	2423
Db	11607	GCAACACAGTCTGCTGGCATCTGAGGCTGAAGGGCTTGCAGGCCAGGCACGGGTGACT	11666
QY	2424	-----	2423
Db	11667	GCGTCCCTCCCAAGTATGATAAACTGGATCATCTCAGAAAGCGAGTCTGACTCAGCT	11726
QY	2424	-----	2423
Db	11727	GCACTTAGAAGAGTCTTCTCTCCCATGCCCTGGGGCCCTTCTGGAGCAGGTGCCTCGAT	11786
QY	2424	-----	2423
Db	11787	GGGTACAGGGAGGATGCTCTGTGTAGCTGGTGAACACAGAGAGGCTGTGACTC	11846
QY	2424	-----	2423
Db	11847	CCAGAAGAAGACAGAAGTTAAGCTCACAGTTTGGACCCACTTTTGTGCTAGGAGGTGT	11906
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	12027	TTGGATCTTGGTTTCTCACTGGAGTGAGTTGTAGGCAGCTAGAGCTGTTTGGAGTGT	12086
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QY	2424	-----	2423
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Db	12567	GCTTGAGTGCATGACTGCTTGCCTTCTACTCTTTGAGTTCTAGTTGTGAGTAGAAGGCC	12626

Qy	2424	-----	2423
Db	12627	CTGTTATGTAGATACATAAGTTGGGAAGATTCTAATGGCCCCAATTGTAGATTCTAATTAA	12686
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Db	12747	GGGGAATTTAATGGCATGATCAGGTGGCAAGGTCCAGAGATGATTACTTAGGGTGGGAGA	12806
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Db	12807	ATGTTACAGGGGTCTTGGACACAGGSCATCCAGGTGGGAATCAGAGGGAGAGGTAGGT	12866
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Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	13047	TAGACACAAGGCTCAGGAGGCTGAGCCATGGAGTTGCTGCTCTTAGCTTAGCCCCATTG	13106
Qy	2424	-----	2423
Db	13107	CAACTTTTAGCTTCCCCAGAGCAAGACACTGTTCCTAAGGCTGCAGGCCACAGCCCCAG	13166
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Db	13227	GGCCATCCCAAGACTTGAATAACGAGGGTGCACGTTTTTTAAATGAAATATTATCT	13286
Qy	2424	-----	2423
Db	13287	TTGGAATTATAAAATAAATATTACATTATAGAGACTGTAGATTAGAGAGCTGCCACCTT	13346
Qy	2424	-----	2423
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Qy	2424	-----	2423
Db	13407	CGCCAGGGGGAGTGCAGTGGCGCGATCTCAGCTCACTGAAAGCTCCACCCTCCCGGGTT	13466
Qy	2424	-----	2423
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Qy	2424	-----	2423
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RESULT 9

AC004241

LOCUS

DEFINITION

AC004241 Homo sapiens, *** SEQUENCING IN PROGRESS ***, 37 unordered pieces.

AC004241 GI:2943840

VERSION

HTG: HTGS-PHASE1.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 148875)

Muzny, D., Aronson, A.D., Brundage, E., Carvelli, K., Chen, E., Di, W.,

Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C.,

Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L., Kampal, R.,

Karpathy, S., Leal, B., Li, Y., Liu, W., Logan, O., Lu, J., Ly, T.,

Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Rowland, K.,

Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J., Vo, Q.,

Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 148875)

Worley, K.C.

Direct Submission

Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

[WARNING] On Mar 14, 1998 this sequence was replaced by a newer

version g1:2960506.

On Mar 7, 1998 this sequence version replaced g1:2920325.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 37 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.

* 1 25614: contig of 25614 bp in length

* 25615 25634: gap of unknown length

* 25635 34177: contig of 8543 bp in length

* 34178 34197: gap of unknown length

* 34198 41767: contig of 7570 bp in length

* 41768 41787: gap of unknown length

* 41788 48861: contig of 7074 bp in length

* 48862 48881: gap of unknown length

* 48882 55534: contig of 6653 bp in length

* 55535 55555: gap of unknown length

* 55555 61786: contig of 6232 bp in length

* 61787 61806: gap of unknown length

* 61807 68003: contig of 6197 bp in length

* 68004 68023: gap of unknown length

* 68024 73983: contig of 5960 bp in length

* 73984 74003: gap of unknown length

* 74004 79554: contig of 5551 bp in length

* 79555 79574: gap of unknown length

* 79575 85092: contig of 5518 bp in length

* 85093 85112: gap of unknown length

* 85113 89598: contig of 4486 bp in length

* 89599 89618: gap of unknown length

* 89619 93940: contig of 4322 bp in length

* 93941 93960: gap of unknown length

* 93961 98201: contig of 4241 bp in length

* 98202 98221: gap of unknown length

* 98222 102007: contig of 3786 bp in length

* 102008 102027: gap of unknown length

* 102028 105662: contig of 3635 bp in length

* 105663 105682: gap of unknown length

* 105683 109134: contig of 3452 bp in length

* 109135 109154: gap of unknown length

* 109155 112546: contig of 3392 bp in length

* 112547 112566: gap of unknown length

* 112567 115593: contig of 3027 bp in length

* 115594 115613: gap of unknown length

* 115614 118360: contig of 2747 bp in length

* 118361 118380: gap of unknown length

* 118381 121101: contig of 2721 bp in length

* 121102 121121: gap of unknown length

* 121122 123793: contig of 2672 bp in length

* 123794 123813: gap of unknown length

* 123814 126440: contig of 2627 bp in length

* 126441 126460: gap of unknown length

* 126461 128728: contig of 2268 bp in length

* 128729 128748: gap of unknown length

* 128749 130921: contig of 2173 bp in length

* 130922 130941: gap of unknown length

* 130942 132882: contig of 1941 bp in length

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* 132903 134836: contig of 1934 bp in length

* 134837 134856: gap of unknown length

* 134857 136559: contig of 1803 bp in length

* 136560 136679: gap of unknown length

* 136680 138364: contig of 1695 bp in length

* 138365 138384: gap of unknown length

* 138385 140065: contig of 1681 bp in length

* 140066 140085: gap of unknown length

* 140086 141663: contig of 1578 bp in length

* 141664 141683: gap of unknown length

* 141684 143007: contig of 1324 bp in length

* 143008 143027: gap of unknown length

* 143028 144350: contig of 1323 bp in length

* 144351 144370: gap of unknown length

* 144371 145640: contig of 1270 bp in length

* 145641 145660: gap of unknown length

* 145661 146696: contig of 1036 bp in length

* 146697 146716: gap of unknown length

* 146717 147464: contig of 748 bp in length

* 147465 147484: gap of unknown length

* 147485 148186: contig of 702 bp in length

* 148187 148206: gap of unknown length

* 148207 148875: contig of 669 bp in length.

FEATURES

Location/Qualifiers

1..148875

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 39613 a 33026 c 33606 g 41869 t 761 others

Query Match 44.3%; Score 1077.81; DB 8; Length 148875;

Best Local Similarity 10.1%; Pred. No. 7e-49;

Matches 1587; Conservative 0; Mismatches 482; Indels 13704; Gaps 22;

Qy 1 CAAGGATCCGATGGCTATATGAGTGTGAGGTGAATGATCATTCATGTGGAAGATGCAG 60

|||||

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Qy	61	GGGTTTTTTCAGACCGAGGTTTTGGAAGAGAGATTTCAGACATGCTGGTAGTTTTTGGGAAATCA	120
Db	133050	GGGGTTTTGAGACCGAGGTTTTGGAAGAGAGATTTCAGACATGCTGGTAGTTTTTGGGAAATCA	133109
Qy	121	CCCATGTGACGGCGACACATGAGCGCAGTAAAGAACTCTGCAGGGGTCCCTTGAGATTTGGA	180
Db	133110	CCCATGTGACGGCGACACATGAGCGCAGTAAAGAACTCTGCAGGGGTCCCTTGAGATTTGGA	133169
Qy	181	AATGTAGGGAAGACCAATGATTGAGGTCCGAACTCTGGAGGATCTGCTATACCAGAGCT	240
Db	133170	AATGTAGGGAAGACCAATGATTGAGGTCCGAACTCTGGAGGATCTGCTATACCAGAGCT	133229
Qy	241	GGGAGGAGGACAGAGTCAGTACCAGAGTCGGAAAAAGCAGGCTGGAGGGGAACCTG	300
Db	133230	GGGAGGAGGACAGAGTCAGTACCAGAGTCGGAAAAAGCAGGCTGGAGGGGAACCTG	133289
Qy	301	AGTCAGGAGACTTGCCTGGCAGCGCTGCCCTGCCAGCAGAGCGCTGCACAGTGGTTTCCA	360
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Qy	481	GTTACTTAACCTCTCTGAGCCTCATTTATTTATCCATATAAATGGAATAAAAAATAATAC	540
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Qy	841	GTGCTCCTGGTGACACAGGACCTCACAATCCCTCCACGGTCTCCTCTCATGTCTCT	900
Db	133830	GTGCTCCTGGTGACACAGGACCTCACAATCCCTCCACGGTCTCCTCTCATGTCTCT	133889
Qy	901	CCCAGCCTATTATTCTCGTTCTCTCTTCCCTCCAGGCCGGAACTTGCCTTGGTCTCC	960
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Qy	961	CAACCAAGGACGAGCCCTTCTGGCAGCAGCTGTGCCATCCCAAGTTGGGGATAAAG---	1016
Db	133950	CAACCAAGGACGAGCCCTTCTGGCAGCAGCTGTGCCATCCCAAGTTGGGGATAAAGTTG	134009
Qy	1017	-----	1016
Db	134010	GTGGTCTGTCCGGCTGGGCACAGCCGACATCTGCACCCCTGCTGCTCTCTCTTG	134069
Qy	1017	-----	1016
Db	134070	TCTGTCTGTCTACTTTTGACCTCGGTGTGCTTGGCCCAAGGTGGCAGCTGTACTCT	134129
Qy	1017	-----	1016
Db	134130	CAGGGTCTGTGTTCCAGGCTGCTGGCTAGATCTGCCCTTACCTGCTCTTTTGTGCTCA	134189
Qy	1017	-----	1016
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Qy	1207	-----	1206
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Qy	1207	-----	1206
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Db	138510	TTTTCTCTGTTCTGACATAAACATCACCTGCCATATCAAAACCTTTTGTAGTTCAGAAAGTC	138569
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Db	140250	GGGATCTTGACTCACTGCAACCTCCGCTTCCAGGTTTAAAGGATTCCTGCTCAGCC	140309
QY	1270	-----	1269
Db	140310	TCCCAGTAGCTTGGACTATAGGCACACACCACATGCCAGCTAATTTTGTATCTGTA	140369
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Db	140370	GTAGAGATGGGTTTACCATGTTGGCCAGGATGCTCGATCTCTTGACCTCGTGATCC	140429
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Db	140430	ACCCCTTGGCTCCCAAGTGTGGGATTACCGGCTGAGCCACCGACCTTGGTCTAA	140489
QY	1270	-----	1269
Db	140490	TTTCTTACCAAGTTCTTCTGAGGGAGGAAATGGGCAGTAGATCTGATGCCAGGAAAC	140549
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Db	140550	TTTGGCTTATTCGGTTCTCTCGACCCAGTACTCCAGAGTGGGATTTGGGGTGGG	140609
QY	1310	CTGGACCTGGTGAGTGCCAAGA	1332
Db	140610	ATGGCTCTGCTCTATGCTGGGAAGGGGACCTTAGCCCTAGCCTTCTTCTGTTTACCC	140669
QY	1333	-----CCTGGCAGGCGCTGACGGAC	1354
Db	140670	ACATCTCCCTCCCTGCCCCAGCCAGTGTCTTGGATCCAGCCTGACTGACCAGGTCTGAGAG	140729
QY	1355	CACGACTGGAGCCTCT	1370
Db	140730	ACAGAACTGGGCACTCTCTAAAGCAGGAACAGGGCCCTGCTTAGGACCCCTCTTTACAGCT	140789
QY	1371	-----	1370
Db	140790	CCTGCACTGCCCTTACCAAGACTCTGAAACAAAAGAGACAAGTGGGCACAGGTTTGAG	140849
QY	1371	-----	1370
Db	140850	TCCTGAACAGAGCCTGGCCCTGGGATGAGTTGGAAGATGGGACACTTAAGACAAAAGT	140909
QY	1371	-----	1370
Db	140910	TTTGGAAAGTGGGAAAGTTGCAAGAGGGAGTGTGGGAGGTAGTAGTGTGGG	140969
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Db	141030	CACAACTGGAATGGGCAGCCATTTCAGAACACTGATCAAGGTGATGATGATGTC	141089
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Db	141090	TCCTGGGACCCACACAGACACACACACACACATACATGCTCTCTCTCTCT	141149
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Db	141210	AACTTGGCGGGGAGCAGCTGCTCCCTCCCTTCTTAGGGACCTCTCCAGCCCTGCCCTG	141269
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Db	141270	TTGCTGCTCTCTTCTGGCTTCTCTACCTCTGCTTACCTTCCCTCAGCCAGCATCACACC	141329
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Db	141390	CCAGAGGAATGTGCTCCAGGAGAGTGTGGGGTTCCTGCTTTTCACTCTGCAACTTCTG	141449
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Db	141450	CAGCTCCAGCCCTGACTGTGAGCCCAAGCTTGCCCAATTTGGCTTACAGGAGGACAG	141509
QY	1457	-----	1456
Db	141510	AGCCCATCCCTCTCTCCCTCCCATCACTGTCTAAGTGGCTCATGAGTACTGTTGTG	141569
QY	1457	-----	1456
Db	141570	ACCTGTTAGTCTAGGAAGGTTTGGCTTGGGGCCCATTAAGGCTCCAGCTCCCTGCCCT	141629
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Db	141690	AGTTTCATCATCTACAATAATTAGTGAGCATAAAAATACAGCACTTGCCTGTATTTTAAATG	141749
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Ds	141810	TAATATTTTCAAAACATATATTTTGATATATTTGGTTTCCCTTTGTAACTCTAGTTGTACAG	141869
Qy	1457	-----	1456
Ds	141870	TAAAGCATTTAAAAATATCTGAGAGCGTTCAACATACAGCTAAAGGGGAATTCATGGC	141929
Qy	1457	-----	1456
Ds	141930	ACTGAGAAGTTTCGAATTCCTATTTATCTATTTTACAGGCTTTTAAAAATTCGGCAAT	141989
Qy	1457	-----	1456
Ds	141990	AGTCTGTAAAGTATAACAAGAGAAACAAGCTTAAGTCTAAGTTTCTGCCATCGGATATA	142049
Qy	1457	-----	1456
Ds	142050	ATTCTACTGATTTCCAACTTGGGCACAAACAGAAAAAGCTGTTAATATAGGATCAAAAT	142109
Qy	1457	-----	1476
Ds	142110	TTTTTTTACATATGTTTATTAATCAGCAGTTTCAATGACAGCAGTTCTCTTTTGGTATACA	142169
Qy	1477	-----	1476
Ds	142170	TGTGTGTATATGAACATGTCAGATAAGACTTTGCCAAGGGGCTCTGCAAGTGAAAC	142229
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Ds	142230	TAAATTTCAATCAACATCCAGAATACTATATATAAAGCGACTAGAGACAAACTGGTAAAC	142289
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Ds	142350	CCCTGTGGCTTGAACATGATATACACAGGTACCTTAACACACCCCATACACATGCACACA	142409
Qy	1477	-----	1476
Ds	142410	CACACACACACACACACAGCGACTACTTTGCCCTCTCAGATCACGTTCAATTTAAATG	142469
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Ds	142470	CTCAAAAATCACGTAGATTAAATGTTGACTGACCTGAATATATACCAAAAATGGCCACGTGA	142529
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Ds	142530	GCTAACCTTACAGCCCATGATGGCATATCCGGTAACCTTCTGTGTACACGTTGCCCCAGTT	142589
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Ds	142590	CTAGAAAATCATTTATCCGGATCAGACTCCCATGTAAACCAAGACTTGCATCCGAATCCCTC	142649
Qy	1477	-----	1476
Ds	142650	AGATAAGGCTCGCTCGGTAGCTGGAAGAAGCGCAATTAGCACCATCTGCTGCTATACCT	142709
Qy	1477	-----	1476
Ds	142710	CGAGTAAAGCAATCAATAGTCTCTTCAATAATCCCTCTCTTGACACATCCAGTCCCTCTG	142769
Qy	1477	-----	1476
Ds	142770	TACTTTGTACGAGATATCAGGATAGGAGAAGCATCTCAANTAAATACATAGACGAGTGCAG	142829
Qy	1477	-----	1476
Ds	142830	CACCCCGACACACTGCAAGGATACCCACGAGTATATCTCGTCAGCCATACCTTAAG	142889

Db	145862	TTCTCTGAGCTCCACAGCACTGGCCACCAGGAGCCCCGTGGGCCTCAGGGGCCAACTC	145921	Qy	2247	-----	2246
Qy	2045	CAGC-----	2048	Db	146952	TAATTTGTTATTTTGAAGATGATGTCACCATTTTATTTTGTCTGTTGTTTCATT	147011
Db	145922			Qy	2247	-----	2246
Qy	2049	-----	2048	Db	147012	TTTTTGGCCTTCCTGTGTGTACTGTAATATATTTTGAATTCACACTTTGATTGGTCTAT	147071
Db	145982	ATAAAGGCCCATTTAGTCAGGGAGTGGCGAGGAGGAGGCCACCTTAGGCCCTCTGCGC	146041	Qy	2247	-----	2246
Qy	2049	-----	2048	Db	147072	ATAGTTCTGAAAAAGATATATGCTTAATTGTTTGGGTGCTGAGGTATTTACATTAATAGT	147131
Db	146042	CTCTGCGACGGCCTGGCCACAGGCAACCATGTCAGCAAGGGCCCGGTGAACACCTATCA	146101	Qy	2247	-----	2246
Qy	2049	-----	2048	Db	147132	ACATTACTTATTGCAGTCTACTGTGTATTTACCAGTTTCAAGTGAAGTATAGAAACCTT	147191
Db	146102	GAGACCAAGGGTGTGTCTGTGGAGGAGAGCTTCCCACGCCACAGAGCCCCCTCAGGGT	146161	Qy	2247	-----	2246
Qy	2049	-----	2048	Db	147192	ACCTTCCCTTTTGTCTGTCTCATCTCCTCTACTAGTTGTCTTAAATATTTTCTGTACATA	147251
Db	146162	CAGGGCGAAGGAGGGCCTGCAGTCCAGGAGGAGAGAAAGAACTGGGGCCAGG	146221	Qy	2247	-----	2246
Qy	2049	-----	2063	Db	147252	CATTTAGAACCCACATAGGACAATGCCGTGATTTTGTCTCAACCTTCAAAACATAAATTAG	147311
Db	146222	CAGACACCTTCATCTGAGGAGATGCATTTCCACAGCCATTTCTCAACCTTCAGACAAGAG	146281	Qy	2247	-----	2246
Qy	2064	ACAAACAGCGGAACTCTCCCGCTCTCCGAGAGCTGGAGCCATGAGAGGGGCTGGGA	2123	Db	147312	AAAACTCAAGAGAAAAAGAAACCTGTTGTAATTTGTCATAGTTTTTGTCTTACTGTGTT	147371
Db	146282	AGAAGGAGGTGAGTGAGCCAGGTATCCCTGGGGTGCAGC-----	146323	Qy	2247	-----	2246
Qy	2124	CTGGAGCTGAGCAGGCACTTTCAGCGGGAAGCCAGGCTGTCGGGGCCCAAGATACTC	2183	Db	147372	CTTTCTCCTTAATGTTTCAAGTCCCTCTTTTATTTATTTTGTCTGTTTGTAGAACTTC	147431
Db	146324	-----	146351	Qy	2247	-----	2246
Qy	2184	ACAGGCTGGCCACAGCTGGGCAAGGCTCTCCGTGGAGTGGACTCGAGTCCCTGGAGCAGG	2243	Db	147432	CTTTACCCATTTTTTTGGGTGAAGAATACTTTNNNNNNNNNNNNNNNNNNNNNNNNNNNN	147491
Db	146352	CCCGCCCTCACCAGTGGTTTCACAGTTAAGCAGCAGCAGGTAAGTATCACATTAAGAAGG	146411	Qy	2247	-----	2246
Qy	2244	CAG-----	2246	Db	147492	TNTGTCCATCCTCTAGGTATAGCAAGCTGAACCTGCCATGTACCTAAGATTGATCATCC	147551
Db	146412	GAGAACACGGTCTTTGAACACAGGCCCCCGACACTTTGTGTAATTTTCAAGGCCAGGAGGGA	146471	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147552	AAAGCAACGCACATCAACCGCAGCTGCCATAGCCAGTAAGCCACAACTTGAAGCGG	147611
Db	146472	AAGAAAAAATTAGAGCAGATCGACCCAGGGTTTTCAAGTAAATACTTTGTTTCAAA	146531	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147612	CTGCAGATTGTAGCTCACCTGAATGACCAGCATGCCATTTTCAGCCTAACCTCCGGTGATC	147671
Db	146532	TGAAGCTCCAAACCCCTTTTGGAACTCTCAGGCTGCTCCCGGTGGGAAATTTATATGG	146591	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147672	CAAACTACTCCAACGATAAATACTATATGAAATTCGCTGTGTATGTATGATTCATGCAT	147731
Db	146592	CAGAGTTGAAGNTTAAAAATTTTAGGAAAAATTTGACGGCGGGGAGATTGGGCAG	146651	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147732	ATCAGCCCATCTACTTCGGCTCCAATAGCAAAAGTTATCCCTGTATACCAATTGGGAATGA	147791
Db	146652	AAAAGCTTGGACATTTGAGGGGTGTGTTTGTAGTAAATATAAANNNNNNNNNNNNNN	146711	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147792	TATGCACTAAAGCCTTAGGACATTTGCAATTTCAAACTTTGGGGTACTGATGACTCCATCT	147851
Db	146712	NNNNNTTGGTAATTTCTTTGCTCTGAAGTCTACTTTATCTGATATTAATGTAGCCATCC	146771	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147852	CTAAATTTCAAAACTGACCATAGCAACTCCCAAGCTTAAAGTCTCATATCCAGGAATGATA	147911
Db	146772	TTGCTTTTCCCTTGATTAAATTTTGCATGATATGCTTTTTTCCATCTTTCACCTTCAGTC	146831	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147912	TCATTTGGACATATTCATAGACAAATATTTAGCATTTGCCGTAATTTACAATCCTTTTATA	147971
Db	146832	CTTTTATATAATTAATTTGAAGCAAGTTTGTATATAGACAGATATAGTTGGGTATGTT	146891	Qy	2247	-----	2246
Qy	2247	-----	2246	Db	147972	ATATGTACCCAGCATCACTACTACACTGGACGGTATCGGAGTTTACATTTCCCGACCAAT	148031
Db	146892	TTGCAACCAACATGCCATCTCTGCTCTTTTAAATTTGTTTATAGACCAATTTACATTAACA	146951				

QY	2247	-----	2246	*	16424	19637:	contig	of 3214	bp in length
Db	148032	CAGTGTGTAGAGGGTACTTTTAATCATTAGGCTTTTCTGTGACCCCTCAGCGAATCCTA	148091	*	19638	19657:	gap of	unknown	length
QY	2247	-----	2246	*	19658	22807:	contig	of 3150	bp in length
Db	148092	TATACATAATCTAACGAGGTGATCCTTTGGCTCGTGAATTCGCCAGTTTTGAATTTAC	148151	*	22808	22827:	gap of	unknown	length
QY	2247	-----	2246	*	22828	25888:	contig	of 3061	bp in length
Db	148152	GTTTATCGGGAAATCAGGATATTCACCTTCCCTNNNNNNNNNNNNNNNNNGGCC	148211	*	25889	25908:	gap of	unknown	length
QY	2247	-----	2246	*	25909	28740:	contig	of 2832	bp in length
Db	148212	GCCAAACGACTGGGATGGTAGTTCATCACCTGGTGGCTCCACCGTGTATCCAGCT	148271	*	28741	28760:	gap of	unknown	length
QY	2280	GCTAGGAGGACCTCGGAGTGACCCGAGCGAATACGAATGACCAAGCCCAAGGA	2339	*	28761	31494:	contig	of 2734	bp in length
Db	148272	GCTCGGAGG-----CTGAGCGAGAGAACTCACTTGAACCTAGG-----	148310	*	31495	31514:	gap of	unknown	length
QY	2340	AGGAGGACAGAGAGCCCGAGGTGGTGGAGAGTGAGTGCCTGG-----	2389	*	31515	34166:	contig	of 2652	bp in length
Db	148311	-----AGTGGAGGTGCGAGTGAGTGTGCGTGGCCAC	148344	*	34167	36734:	contig	of 2548	bp in length
QY	2390	-----ACGTTGTGTCAATAGAGAGTCTCCACACAGCAAAAAA	2434	*	36735	36754:	gap of	unknown	length
Db	148345	TGCACCTCCAGCCTGGCGACAGCAGCAAGACTGTCTCAAGACAAAAACAA	148397	*	36755	39243:	contig	of 2489	bp in length
RESULT 10	AC004241	116389 bp	DNA	linear	HTG	28-FEB-1998			
LOCUS	AC004241/c	116389	bp	DNA	linear	HTG	28-FEB-1998		
DEFINITION	Homo sapiens, *** SEQUENCING IN PROGRESS ***	69	unordered	pieces.					
ACCESSION	AC004241	GI:2920325							
VERSION	HTG; HTGS_PHASE1.								
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.								
REFERENCE	1 (bases 1 to 116389)								
AUTHORS	Muzny, D., Aronson, A.D., Brundage, E., Carvelli, K., Chen, E., Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Ganes, R., Garcia, C., Goodman, M., Gorrell, J.H., Haywood, M., Jackson, L., Kampal, R., Karpathy, S., Leal, B., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Rowland, K., Savage, L., Scherer, S.S., Shen, H., Timms, K.M., Todd, J., Vo, O., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.								
TITLE	Direct Submission								
REFERENCE	2 (bases 1 to 116389)								
AUTHORS	Worley, K.C.								
JOURNAL	Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA								
COMMENT	[WARNING] On Mar 7, 1998 this sequence was replaced by a newer version q1:2943840.								
	* NOTE: This is a 'working draft' sequence. It currently								
	* consists of 69 contigs. The true order of the pieces								
	* is not known and their order in this sequence record is								
	* arbitrary. Gaps between the contigs are represented as								
	* runs of N, but the exact sizes of the gaps are unknown.								
	* This record will be updated with the finished sequence.								
	* as soon as it is available and the accession number will								
	* be preserved.								
	* 1 4643: contig of 4643 bp in length								
	* 4644 4663: gap of unknown length								
	* 4664 9082: contig of 4419 bp in length								
	* 9083 9102: gap of unknown length								
	* 9103 12816: contig of 3714 bp in length								
	* 12817 12836: gap of unknown length								
	* 12837 16403: contig of 3567 bp in length								
	* 16404 16423: gap of unknown length								

* 89649	89668: gap of unknown length	116318	GGCAAAAAAGGGAATTTCCAGGCACCTCTAAAGAAATTCCTTAACAGTGTATCTCAGACA	116259
* 89669	90819: contig of 1151 bp in length	QY 79	-----	78
* 90820	90839: gap of unknown length	Db		
* 90840	91979: contig of 1140 bp in length	Db	TGCTATATGGAGAATACTGGGTAAATCACAGGTACTACCTTCAGAGAGCTTTCTGTATTTG	116199
* 91980	91998: gap of unknown length	QY 79	-----	78
* 92000	93133: contig of 1134 bp in length	Db		
* 93134	94260: gap of unknown length	QY 79	-----	78
* 93154	94260: contig of 1107 bp in length	Db		
* 94261	94280: gap of unknown length	Db	ACAAAGGTCATTTTTCGAACTGAAATGATATCTGTAGTGTATTTTAAAGAAAGATGCATTA	116139
* 94281	95382: contig of 1102 bp in length	QY 79	-----	78
* 95383	95402: gap of unknown length	Db		
* 95403	96468: contig of 1066 bp in length	QY 79	-----	78
* 96469	96488: gap of unknown length	Db		
* 96489	97546: contig of 1058 bp in length	Db	TTTCCCAACCAATCAGAAATTTGGTTCAAATTTCTCATGTTACTAAGTACTAATGACCTG	116079
* 97547	97566: gap of unknown length	QY 79	-----	78
* 97567	98618: contig of 1052 bp in length	Db		
* 98619	98638: gap of unknown length	Db	AATATCTCCTCTCATTTTTCAGTTTCTCACTCTGTAATAGGCATTAATATGCTCTGTGG	116019
* 98639	99685: contig of 1047 bp in length	QY 79	-----	78
* 99686	99705: gap of unknown length	Db		
* 99706	100746: contig of 1041 bp in length	QY 79	-----	78
* 100747	100766: gap of unknown length	Db	CTTTAGTGAGCAAGAGGTAGTGTGTTTAAAGCTCATAACACATTTTGTTCACATTATAA	115959
* 100767	101785: contig of 1019 bp in length	QY 79	-----	78
* 101786	101805: gap of unknown length	Db		
* 101806	102820: contig of 1015 bp in length	QY 79	-----	78
* 102821	102840: gap of unknown length	Db		
* 102841	103781: contig of 941 bp in length	Db	ATTCTAAGCCTCTCTATTATTTCATAAAATAGGTTTGTGATTACAAAATCACAATCTGA	115899
* 103782	103801: gap of unknown length	QY 79	-----	78
* 103802	104734: contig of 933 bp in length	Db		
* 104735	104754: gap of unknown length	QY 79	-----	78
* 104755	105659: contig of 905 bp in length	Db		
* 105660	105679: gap of unknown length	QY 79	-----	78
* 105680	106576: contig of 897 bp in length	Db		
* 106577	106596: gap of unknown length	Db	TTTTTGACAGAGAGTCTTGCTTTTCCACCACAGGCTGGAGTGCATGCTGATCTCTGC	115779
* 106597	107482: contig of 886 bp in length	QY 79	-----	78
* 107483	107502: gap of unknown length	Db		
* 107503	108379: contig of 877 bp in length	QY 79	-----	78
* 108380	108399: gap of unknown length	Db		
* 108400	109276: contig of 877 bp in length	Db	TCACAGCAACCTCCGCTCCCGGGTTCAAATGATTTTCTGATGAAGTACTTTTTNNNNNN	115719
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* 109297	110163: contig of 867 bp in length	Db		
* 110164	110183: gap of unknown length	QY 79	-----	78
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* 111040	111867: contig of 828 bp in length	Db		
* 111868	111887: gap of unknown length	Db	AATTAATTTTCTCTGAAATTAATTGAGGCTAGTTTGGCCCTACCATATAGCCAACCTT	115599
* 111888	112681: contig of 794 bp in length	QY 79	-----	78
* 112682	112701: gap of unknown length	Db		
* 112702	113453: contig of 752 bp in length	QY 79	-----	78
* 113454	113473: gap of unknown length	Db		
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* 114242	114974: contig of 733 bp in length	Db		
* 114975	114994: gap of unknown length	Db	CCTGTATATATCTGTAAAGTCAATTTGTTCCAAAGGTATAGTTAAACCCATGTTCTCTTT	115479
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* 115706	115725: gap of unknown length	Db		
* 115726	116389: contig of 664 bp in length.	Db	GTAGACTCTCTGCTTTGATGACCTGCTGTGAGTGGAGTATGAAGTCCCCACATATTAT	115419
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source		Db		
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/mol_type="genomic DNA"		QY 79	-----	78
/db_xref="taxon:9606"		Db		
BASE COUNT 31387 a 25231 c 26322 g 32017 t 1432 others		QY 79	-----	78
Query Match		Db		
Best Local Similarity 2.28; Pred. No. 1.7e-17; Length 116389;		QY 79	-----	78
Matches 1440; Conservative 0; Mismatches 823; Indels 62364; Gaps 37;		Db		
QY 50 GAAGGATCGAGGGGTTTTTGAGACCAGG-----		QY 79	-----	78
		Db		
Db 116378 GGAGGTTTCAAAGGCTTTTCCAGACCAGTCTCCCGAATTCCTTCCAAATCTCGAGA		QY 79	-----	78
116319		Db		
QY 79 -----		QY 79	-----	78
TCTGATATAAGAATGGCTACCCCTGCTGCTTTTGGTATCCACATGCAATGCCTTT		Db		
115179		QY 79	-----	78

QY	79	-----	78	QY	79	-----	78
Db	115178	TTCCACCCCTTTAAGCTTATGAGTCTTTACGTGTAGATGAGTCTCTGGAAGCAGCA	115119	Db	114098	CAACAGGTTTTCTTTCTTCTTCTGAGTTTTCTAAATATATGTTTGAAGGTTGAAGCAAAA	114039
QY	79	-----	78	QY	79	-----	78
Db	115118	GATGGTTGGTGAGTTCTTATCCATTCTGCAGTCTCTTATCTTTGAAGTGGACATTTAGG	115059	Db	114038	TCACGGCAATGTCTCTATGTGTCTTAAATGTATGTACAGGAAATATTTAAGACAACTAGT	113979
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Db	115058	CCATTTACAGTCAATGTATGTATGTAGATGTGAGTACCCATTGCATTTCTGTGAACATAT	114999	Db	113978	AGAGGAGGATGACAGAACAAAAAGGAAGGTAAGGTTTCTATCTTCACTTTGAACCTGGTAA	113919
QY	79	-----	78	QY	79	-----	78
Db	114998	TGTANNNNNNNNNNNNNNNATCTGGTGTGGCCCATTTTTTATCTTAAGGCGTTT	114939	Db	113918	ATAACAACAGTAGACTGCAATAAGTAATCTACATATAATGTAACTACAGCACCCAAA	113859
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Db	114938	TCCCTATTGATTATATTTTGAAGAGGTCCTATAAATCTGGAATAACCTAATCCTTTTAGCC	114879	Db	113858	CAATTAAGACATATACTTTTTTCAGAACTATATAGACCAATCAAAGTGAATTTCTAAAATA	113799
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Db	114878	TTTTCCCAATAAFAACTCCTCTCAATTTGTAGCTTAATCTTTATGGAATTTTAA	114819	Db	113798	TATTACAGTAACACAGAGGAAGCAAAAAAATGAAAAACACAGAAAAAATAAATA	113739
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Db	114818	TGAATAGAACATTCNAATGGTTAATATATTTCAACTTCTTGATTTTTTAAAAAGATTAGG	114759	Db	113738	TGGTAGACATACATTTCTAAATAAACAATTTATGTTTAACTGTAATGGTCTTAAAAACAATT	113679
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Db	114698	CTAATTTCTTAAACATTTTAAAGATTTTACATTTTTCACATTTAGGTGTTTTCACATATGC	114639	Db	113618	AAACTTGCTTCAAAATATAATTTATAATAAAGGACTGAAAGTGAAGAANTGGAANAAGACAT	113559
QY	79	-----	78	QY	79	-----	78
Db	114638	TGAAGTTTTTCCAGCTCTATTTTGGAAATAGCCCTACTTTCCCGCGTGATCGCCGTG	114579	Db	113558	ATCATGCAAAACATTAATCAAGGAAGCAAGGATGGCTACATTAAATATCAGATAAAGTAG	113499
QY	79	-----	78	QY	79	-----	78
Db	114578	CTACTATTGTCATATGTCATGTTTGCCGAGATCACTTTCTCATCTCTGTCTTTACACTG	114519	Db	113498	ACTTCAGACAAAGAAAAATTACCAANNNNNNNNNNNNNNNNNNNNNNNAAGATTGTTTCATCA	113439
QY	79	-----	78	QY	79	-----	78
Db	114518	GTCTGTTGCCGTGCTTACATCCATTCCACACTATCTTTAAATTTATATAGCATTTGTAATT	114459	Db	113438	CTCCTTTCTCCTTCCCCTCCACTTCCCTGTGAAGCCCTGAGGCAGGCTGTGGCCAGGCT	113379
QY	79	-----	78	QY	79	-----	78
Db	114458	GTAAGTCTTAATATTTAGTGTAATCTCATATTTCTCCTACCTTTTATTTATTCAGGAATGTCT	114399	Db	113378	CAGGCCCTGACTGTGGGGTACACACCAGGGAGGGCCACGCCCTCCCCACAGAGGGGTGGA	113319
QY	79	-----	78	QY	79	-----	78
Db	114398	TGGGTATTCTTGGACTTTTACTCATCAATATAACTTTTAGAATCATCTTCCCAAAATTCGT	114339	Db	113318	GTGGTCAGTGGAGCCAGCACCCCTCTGCTTTTTCAGCATCTCCGCCCTGGAGCCAGCTGTCC	113259
QY	79	-----	78	QY	79	-----	78
Db	114338	TAAATATCCTGTGGGATTTTGATTAGAAATTGCATTAGATTTATAAATCAGTCTGGAGA	114279	Db	113258	CCTCTCTCTCAGGCTCCATCCGAACAAAAAGGAAGGAGAGCCTGAGATCCGGCACCCCAT	113199
QY	79	-----	78	QY	79	-----	78
Db	114278	GAATCATATGTATGTTTGGTATGATGAATGCTNNNNNNNNNNNNNNNNNNNNNNNA	114219	Db	113198	CCCCCTCCACTCAGCACTCAGTTAGAGCTGGGTGGGGGCATGTCTCCCTTCACACGCTGC	113139
QY	79	-----	78	QY	79	-----	78
Db	114218	GTAGTCTTTCACCCAAAAAATGGGTAAAGGAAGTTCTCTAAACAGAAAAATAATAA	114159	Db	113138	CTTATGGCTTCTGTGTCTCCAACAGCCCTCAGCCTCTGGCTGTCTCTCTTCCCAATPAGTC	113079
QY	79	-----	78	QY	79	-----	78
Db	114158	AAAGAGGACTTGAAACATTAGGAAGAAAGAACACAGTAAGCAAAAAAATATGAACAAATA	114099	Db	113078	ACAAGATTTACCATGATAATAATAGGTTAAGACTTGAATGGTGTTCATCTCTTTTCAT	113019
				QY	79	-----	78

Db	113018	CTTCACCCGTCTCAGCTTACGTTATTTTATCCTGATGACAGAATAGGTACTACAGTA	112959	Db	111938	CTTATGAGTTTAATCGACTCTCAAAAGAGTTACAGGAAGAACTCGCAGGANNNNNN	111879
Qy	79	----- 78		Qy	79	----- 78	
Db	112958	TTTTACTCTGGTTTACAGTCAAGAAGAACTGAGGCACAGCAGGTTTGCCCAAGGTAC	112899	Db	111878	NNNNNNNNNAGTAAATTTTCTGCTAAGATGAAGTTTGCAGCCACCAACCAATFCCAAT	111819
Qy	79	----- 78		Qy	79	----- 78	
Db	112898	ATAACTGCTTAATAGCAGGTTAGACAGGTGAAGTAACTGGATGTGTATCAGCCATGCCCT	112839	Db	111818	AACTTAATTGTTCAAGCAAGAGAACTGAGGCCCAAGCACAGATTGTCCAAGCCCTCTC	111759
Qy	79	----- 78		Qy	79	----- 78	
Db	112838	TTCCCATGCCCCGGCACTCCCATGACAGCTCTGTAATCCCAACATTTTATCTCTTT	112779	Db	111758	AGCCTCTTTGTGGCAGAGTCCAGGTCTTTGACTCTGTGATGGTGTGAGCAGAGCTGCAG	111699
Qy	79	----- 78		Qy	79	----- 78	
Db	112778	GCAGGATTAGACCAAGCATATAAATTCCTTTTCCCTCTCTCGATTTCGGACATCTCTTT	112719	Db	111698	CCCCAGTCTGCCCCCAGGCTGGTGGCCCCATTTTACACTTTTGCTGGCTGGCGATG	111639
Qy	79	----- 78		Qy	79	----- 78	
Db	112718	ATATGATCACTACTTCCNNNNNNNNNNNNNNNNNNNNAAGCACATTTATGAGGGTATCCCC	112659	Db	111638	AAGCACAGGGAGTAGAGTGCAAACTCAAACTCAGGGCTGTGCCGATGAAGCAGAGACCC	111579
Qy	79	----- 78		Qy	79	----- 78	
Db	112658	GCCAGTAAACGAACCTTGTACAGCATAAACGGGTACAGGATCCCTCGCCAAAAGCAT	112599	Db	111578	ACTTCTTATAGTAGCCGTCCACGTGAATGCAATGTCAGACATCGGGTAAGAAATCC	111519
Qy	79	----- 78		Qy	79	----- 78	
Db	112598	AAAAAGTTCGAACACTTATAAGCACAGGAATTTTACCCTGCAATAGTGAAGCCGGTAC	112539	Db	111518	CACTGTGGAGGAAGGCAGAAAAGGGGTCTGTGTAGTGCACAGAGTGGAGTAGAAG	111459
Qy	79	----- 78		Qy	79	----- 78	
Db	112538	AGGAATGAAAAATTTTATGGTTCCCGGCTCGAGTTTCTGCCATCTTAGAGAACGTAG	112479	Db	111458	GGTCCCAATGGCAACAGTCAGACAGTATTTGTTGAGGGTCCATTAGGGGCTGTGTGAA	111399
Qy	79	----- 78		Qy	79	----- 78	
Db	112478	GGTTGCGGTTTATGTCACGACCAGGAGATCAGCGTTCAGGAAGCGCAAAATTTAGCGA	112419	Db	111398	CTTCCAGGAGACTGGATTCTTTAAATAGAAGAGCGAGTCTGCTTTGCTTAAGGTGTCTG	111339
Qy	79	----- 78		Qy	79	----- 78	
Db	112418	AAGACGTTACAGACAGCATTCAGCACAGCATTCGAGAAATAGTCTCGTTTGTATGCGAA	112359	Db	111338	AGCCCCCGGACCCCTCTGCTGGAGTGCAGTGCACATCTACCAGAAAAGGCCAAATC	111279
Qy	79	----- 78		Qy	79	----- 78	
Db	112358	TGAAATGATGGATGAGTCAGAGGATATTGCAGCCAAAGAGGCTGTCTCAGCGCA	112299	Db	111278	ACTATCCATAGGATCCACCTCTGGATATCAAGGATATCACTGTTCACAGTGGCCCTCACA	111219
Qy	79	----- 78		Qy	79	----- 78	
Db	112298	AGGTCACGCTGTCTCCAGGCAGCAGTGTCCGGAAGAAATAGTCGCCCTTTTCCCTG	112239	Db	111218	CATGGAAGAGAAGGATCGTTTACTTGCCCCCAAAATTTATTTCTGTGTACCGGCAGCAAGG	111159
Qy	79	----- 78		Qy	79	----- 78	
Db	112238	TGCAGTCGGAATTAACCTTTTCGGACTACAAAAGCTTTGTGTGTTGGCGAGAAATGG	112179	Db	111158	TTTCTGTCTTATAAGTGTATGAAGTTTAGCTCAAACTAGCCAGGCTGAAACTTTTCAGCC	111099
Qy	79	----- 78		Qy	79	----- 78	
Db	112178	GGAACAAGATTTAGAGTTGATCAGCTTATTCAAAACATATCCCCGGAATAAAGACA	112119	Db	111098	ACGTTCTAAGAAACTGAGCAGGAGTAATTACATACTGTGTGGAAGATCTACTGTGCGN	111039
Qy	79	----- 78		Qy	79	----- 78	
Db	112118	TCTTATCCATTGAAGAAATGGCGAAGATGAAGTTAAAAATAAAATCCTCGCTTGATAA	112059	Db	111038	NNNNNNNNNNNNNNNNNNNACCCAGGAGGTGAAGGTTGCAGTGAGCGAGATCCTGCAAT	110979
Qy	79	----- 78		Qy	79	----- 78	
Db	112058	CAAGGAAGCCTCACTACTCAGGATAAAGGTTCTAAGATAAGTCGTTACTGAAT	111999	Db	110978	TGCATGTACGCTAGTGACCAAGAGCAATACTCCATCTCAAACTAAATAATTAATAA	110919
Qy	79	----- 78		Qy	79	----- 78	
Db	111998	TATGGAATTTGAGACAGGATCGCTTTCGAAGGAAGCCGTGAAGGCCGTGCATTTT	111939	Db	110918	ACATAAAGCCTATCTTGCTTGTCTGCTTCTCTGATTAATTTGGCTAGAGAGCAGG	110859
Qy	79	----- 78		Qy	79	----- 78	
Db				Db	110858	CTTTGGGGACTTCTTTTGGTTTATGCCCATTGATGTTTCCAGTCTGCTTGGCTTCTTCCAG	110799

Db	108638	CAGAATGAATTAANGTTAAATCTCAAGATANTATCATTGAGAAATGCAGGGCAATTTATA	108579	Db	107558	AAAGTTATAAAATTAATTTGATTTGTAATTAATTTGATATTTATGATGAACATTTGTCNNNN	107499
QY	207	-----	206	QY	207	-----	206
Db	108578	CTGCTANAGCGAAATATCTGAGACCAATTTGTGGATGCATATAATATGAGTCTCAGAT	108519	Db	107498	NNNNNNNNNNNNNNNAACAGGGAGGACATTTCTACTGGGTTTAAAAATTTGGGAAATC	107439
QY	207	-----	206	QY	207	-----	206
Db	108518	GGCTTTAATACTGAATAGATTTTAACTAGAAATGTTTAAATGAAATAGTTTGTGCAA	108459	Db	107438	CAAAATTTAAATTTGGGAACCGAAATTTTACCANTTTAAANATTTTAAAGCCCTTGGA	107379
QY	207	-----	206	QY	207	-----	206
Db	108458	TAAGTTGCCCTTTAAATTACATTTGCTGGTTTTATAAATGGTTAAATGGGATTCIN	108399	Db	107378	CTCAGGAATTTANCCCTAAAAATAGGAAATTTACAATTTTAAATATCGATACGCCATAT	107319
QY	207	-----	206	QY	207	-----	206
Db	108398	NNNNNNNNNNNNNNNAATPCCGTTGATTACAGAAATAGTAGGATTTGCTGT	108339	Db	107318	AGGTGCATATCATAAATTCAGAGAATAGGTAAAAATAGCCCTTATAAAGCACCCCTCTCAAC	107259
QY	207	-----	206	QY	207	-----	206
Db	108338	GCACCTTTCTTGAATGGCACTCAAAGCCAGACCTGTTCACCTCAAGGAGAAATCTTGGG	108279	Db	107258	TTAAGAACCCAGAACATTTACCATTATTTTGAAGTTTACCTTGATGCTCCTTTCTGTATPCCT	107199
QY	207	-----	206	QY	207	-----	206
Db	108278	ATTGAGAACAGTGAAGAATTGTATCTGGTTGCCCTTTAAAGATTTCTTAAATTTTATG	108219	Db	107198	GTCCCTTGCTCCTCCAGTTAACCACTATCTTTGAATTATATATTTGTCTCATCCTTTTGA	107139
QY	207	-----	206	QY	207	-----	206
Db	108218	TGACACTTCAGCATTTTAACTTCATCTGTTCGAAATPACCAAGTGAGAGGTCAGAGAAA	108159	Db	107138	TTTAAAAAGGTTTATATATATATATATATGTTTCTTAAATATATATAGTATAATATCTGTCT	107079
QY	207	-----	206	QY	207	-----	206
Db	108158	AGAAGATAAAGAGTGCAGGCACCTCAGGCAGTTGCACATGGGTAAACTAAATATTTGGGCC	108099	Db	107078	TATTTTGTAGCTTAAAGTATATCATACTGTGTGTAGTTTCTGTGGCTCACCTATTTAT	107019
QY	207	-----	206	QY	207	-----	206
Db	108098	TCACTAGAATCTTTCTATTGGTTTACTATCTCTTCAGAAATAGTGTAAATGAGGAAGAT	108039	Db	107018	TATATTTTATGATTCATCTCTGTTTGTAGCTTATAGTCTTAGAGCTCTCATTTGTAACCT	106959
QY	207	-----	206	QY	207	-----	206
Db	108038	ATGCCGTGAGTCTGGGGTCTAATTTTAACTTACCCTATATAGCTTGCTTTATTGACATTTTC	107979	Db	106958	GTTATATAGGATAAATTTCTTTTATAGAAATATACCATATATGTGTCTTCTGTGTGCTG	106899
QY	207	-----	206	QY	207	-----	206
Db	107978	AGATACCCCAAGCCAGTGAACACATTCATGATGATCCTGAAGCTGATCGTGGGGAAAT	107919	Db	106898	GATTGTGGTTCGTTCCCTTCTTCCCTTCTCTCTCCCTCCCACTCTTCTTCTCCC	106839
QY	207	-----	206	QY	207	-----	206
Db	107918	GTTTTATAAACTPAGGGCATCCTTTTGGGTGGATGAACCGATGAATCAGGATGAACA	107859	Db	106838	TCCTTCTGTCCCTCTTTTCTTCTATTGCCCCACCTCTGTCTCTTCTTCTTATTTTCAGC	106779
QY	207	-----	206	QY	207	-----	206
Db	107858	AGCAGATTAAATAGGGTTGAGCATAGGCCATAGAATAATATTAATAAACATATAAACTGT	107799	Db	106778	AATGCTATGAACATTTTGTGATCATGTTTCTGTGGTGGGTCTATAAAATGTGTAGATGTT	106719
QY	207	-----	206	QY	207	-----	206
Db	107798	CATCAATGATAAAATATTCTCCGTACTAAACAAGTTTACTGAAATATATCAACAGTCTTC	107739	Db	106718	CAGTTTCACAGGATGATGCAAAAGTAGTTTGTGTTTACACAGTGTGTACAAAGGTAAT	106659
QY	207	-----	206	QY	207	-----	206
Db	107738	TGATCCTTGGCTGGTTCTTTTGAGGAATGAGTCGCTGCATGTTTCTGCCACCTCGG	107679	Db	106658	GGATGAGTTTACATTCCTCATTAGCAGTGTATAATAATACCTATTTCTCTGATGATGCTGTG	106599
QY	207	-----	206	QY	207	-----	206
Db	107678	GATGGAGACCAGTGGGCTCCGGCAGACACTGAGGAGGCACTTGCTAAATGTTCACTGA	107619	Db	106598	GCNNNNNNNNNNNNNNNAACCCCATTTGTGAAAAGAGGGTTTCCAGGGGAAAAGG	106539
QY	207	-----	206	QY	207	-----	206
Db	107618	ATGAAAAGCGAGTAAAGCTGGAGACTGTGTGTGGCCATGCATTGTCCATGAACACCAAGCA	107559	Db	106538	GAAGAAATTTTGGATTATAAAAAAGGCACCTTTTTTAAGGCCAAAAAGCCTTGTGTTCCGC	106479
QY	207	-----	206	QY	207	-----	206
Db	106478	CCCTTGTGTAGAAAAGCCCAAGTTAGGCCCAAGTTAGGCCCAAGTTCTGAAATAAAGTGAACGGAAGACAT	106419	Db	106478	CCCTTGTGTAGAAAAGCCCAAGTTAGGCCCAAGTTAGGCCCAAGTTCTGAAATAAAGTGAACGGAAGACAT	106419

QY	207	-----	206	QY	261	-----	260
Db	106418	TGAGCTGGCAAGGAGCAGAGGCTCCANTACGATTAGAGCTAAGGTGTAACCTTCGGTCT	106359	Db	105338	CAACCCCTCTCTACAATACCTGTCACAACCTACACGAGCACACCCACCAACCGCTAAC	105279
QY	207	-----	206	QY	261	-----	260
Db	106358	CGATGAGTTTGGGAGTGCCAGCAAGATGCCGATGAACCTTGCTTCCAGCCCTGAGCACC	106299	Db	105278	AACAACTTCCGCGCCCAACCCCGATCCCAAGGCCAAACCATTTCTCCACACCCCCACTACC	105219
QY	207	-----	206	QY	261	-----	260
Db	106298	CGCTCTGTGAGGCCCTTAGAGGAGGAAGGGACAGCAGTTTCAGGCTCTGAACCCCTCAT	106239	Db	105218	AACCTTCCACACCTCTCTCTACAACAAGCCACACACTCGAGACCTTCCCCCTACCCAC	105159
QY	207	-----	206	QY	261	-----	260
Db	106238	GGTGCTGCTGTCCAGCTCCACCTGCCAGGCTTCTACCTGCTCCAGGCTCTCGCTCA	106179	Db	105158	CATCCCATGACTTACATCCCCCCCACAAAACACCCCTCTACTCACCCCAAAGAGG	105099
QY	207	-----	206	QY	261	-----	260
Db	106178	AATCCAGGACTCTCTCGTGTGTTGGTGTGTGTGGGTGCTGTGGGGCAGCAGGAAGCGTGCAC	106119	Db	105098	AGCCTCTCAACCGAGCCATGCATCACTGTGCCCTGGCAGCCAGTCCAGCTAGGCACCTGGC	105039
QY	207	-----	206	QY	261	-----	260
Db	106118	ATCAGTGTGAGGTCTTCAAGCCAGCTCTTGGATACCTTCCCTCCCCCATCACTCCCACT	106059	Db	105038	CCAGTTCACTGTACATGGACTTACCCACTGGCACCCCTCGGGATCCCTTATCAAAGCTGA	104979
QY	207	-----	206	QY	261	-----	260
Db	106058	CTTGCTAGGCCCAACCCCAAAATGCATCCTATGTGCCACTCTTTCAGCAATAAACAAA	105999	Db	104978	TGGGATCGTGGAGACCCCCAGCCCTTTTGTCTAGAGCCTGACGGCTGTGCGAGCTTGAAA	104919
QY	207	-----	206	QY	261	-----	260
Db	105998	TATTCACTCAGACACCTGTGCCCGGCATCGCCTTTCCACCCTGCCATCCTGATCAC	105939	Db	104918	AGAAACATGAAGTGGTGAAGTGGGTCAAGGTTGAGGAGCAGGAGAGGGCGGAG	104859
QY	207	-----	206	QY	261	-----	307
Db	105938	CAAAACCACTCAAGGACTGCCTCCTACAGTTGAGAGCCCTAAGACACCCCATCTGTCT	105879	Db	104858	AGGAAGCTGACACACCGAGAGAAAAATAATGGGTGGGAGAGGGAGGTAGTCAAGGCTGAG	104799
QY	207	-----	206	QY	308	-----	307
Db	105878	ACTCAGGGCCAGGTGTGCCATGCCCCAGGTGAACCTGCCCTGTGGGGAAAGAGT	105819	Db	104798	GAGGAGGAGAAGGGTTTAAGCCGAAGCTAGAAGGACTGCTGCNNNNNNNNNNNNNN	104739
QY	207	-----	257	QY	308	-----	307
Db	105818	GAGGAGCTGGAAGGAGCATGAGACATGAGATAAGAACCTGGGAGATGGGAGCCAGG	105759	Db	104738	NNNACCCGCTGCTCATCTAGTCCCTCCTTTTCATTTCCCAATCTTGTCTCCCTTCCCT	104679
QY	258	CAG-----	260	QY	308	-----	307
Db	105758	ATGTGAGCAGCTCAGGAGCCCTGGGAACATCCGCTCTCGGGCTGGGGTCCAGACCTGATC	105699	Db	104678	GTGTATATCCCTGCCCTTTTGGCCACTTGTGGATGGAGAGGTATTGAGGGACCAAGATGT	104619
QY	261	-----	260	QY	308	-----	307
Db	105698	CCAGCTATGCTGTGTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	105639	Db	104618	GCCTGCTGAGCCAGTCTCTCTCCCTGCCCTAAGGTGGGACAGGGCTGGCTAATGGAGAAA	104559
QY	261	-----	260	QY	308	-----	307
Db	105638	CCACTCACACACCCCAACCCCATACCCCACTCTAGATCAACACAATTTACACTCACTC	105579	Db	104558	ATGATGTAATTGATTATTGATGTCTGCCAGGTGTGGGAGTGGGAGTAGTGGCACCAGT	104499
QY	261	-----	260	QY	308	-----	307
Db	105578	CCACACACCTTCCCATACAAACCAACACACACCATATCCACAAACTTCCCAACCCCTT	105519	Db	104498	GCCAAAGATTGGCCCATTTCTGTCTAGGTATACAGTGTCTGGCACCCCAAGAGATCC	104439
QY	261	-----	260	QY	308	-----	307
Db	105518	AAGCCCCCAACACCATTTCCGGCTCCATCCCATACCCCTTGGGACACCTTCTTCC	105459	Db	104438	TAGAGCTTCTTTGGAGGCCATGGGACCAAGATTCCAGTCCCTCATGACCCCAACAGGTAAAG	104379
QY	261	-----	260	QY	308	-----	307
Db	105458	TCCACAACCGAATTATCCAGATCCACACCCCGGTTTCCCACTCCACACACCTTACCCT	105399	Db	104378	GCAAGAGACACCTGCCCTTCTCTGACTCATTTGGTGGTGGTCCATGGAGCCTGGGAGAG	104319
QY	261	-----	260	QY	308	-----	307
Db	105398	CCCCACCCCATCCCAACACATACCTCTTCCCTTAAACACAGCCCACTACAACCC	105339	Db	104318	CCAGTACCTTGCATCTGACGTACCGAATGCTGGATTGGTCTGTACAGAACTTGGCAAT	104259
				QY	308	-----	307

Db	104258	AAGTCTCTTACCTGTCTCTTGGCTTAGTGGGAGCACTATCACAGGGCTGGACACTG	104199	Db	103178	CCCTTCCCACCTTCCACAGTTTGAGCACTCACAGATATTTGGGGTGTCTCTGAGTCCTGC	103119
Qy	308	-----	307	Qy	308	-----	307
Db	104198	CTGGGACTTGCAGGTGGTGGGATGTGGGGAAGGTCTTCCAGCTGTCCATACACCTGTG	104139	Db	103118	AGGAGCAGTCCGGTTCCTTCAGAGGGTCTGTGGGTCTCTCGGGATTCCTGGGTTGTCT	103059
Qy	308	-----	307	Qy	308	-----	307
Db	104138	CTCAGCAGACTTGGCCTCTGAAGCCCTCCTCCCATCCCTCACCCCTGTCTATACAGACAT	104079	Db	103058	CGCAGTCATCTCGAGCTAAATGTGGGATGTGAGCCTCTGTATGCTGCTCTCTCTGTCT	102999
Qy	308	-----	307	Qy	308	-----	307
Db	104078	TCCTCAGCGACTTCTCTCCAGCCACACAGGTCTTTCATGCCAGCGCCAACTCTGGCGTG	104019	Db	102998	GAGTCAGAGCTGCAATCTAGTCTGCTTCTGTCCACCATAATGATCAACAAGTCTTAAT	102939
Qy	308	-----	307	Qy	308	-----	307
Db	104018	CCCTTCTGCACCAATATCCCTTCAGCTCCAGGGGATGGTGTGCATGGGGATAGGATGGT	103959	Db	102938	CCTTGTTAATTTTAAATTTTAAATGTCAGGATACTTATATCAGGTTTGATATA	102879
Qy	308	-----	307	Qy	308	-----	307
Db	103958	GCCTGGGTTGAGAGAAATCTCACCAGGTGCTGTGTGAGCCCTTTAAATGCCAGCC	103899	Db	102878	TAGGTAACTCGAGTCACAGGTGATGATCTATGCGTANNNNNNNNNNNNNNNNNNGT	102819
Qy	308	-----	307	Qy	308	-----	307
Db	103898	TGCTGCCAGGCCAGCTTGCCAGGGCCCTGGGCATCTCTGCCCTCTCTTGGCTCAGGTG	103839	Db	102818	TACCCAGCAAAAATTTGCTGCCGCCCTTTAACTTTCTTAATGAGATCTGCGGCAATCAA	102759
Qy	308	-----	307	Qy	308	-----	307
Db	103838	GGTGGCCCTGCTTGGATGTTGGTTGATGAACCTCTNNNNNNNNNNNNNNNNNNNA	103779	Db	102758	TAAAAATTTAAAGGATCAGTGAGCACTAACCAAGTGAACCCGTTGTCTAGGTACTAGCA	102699
Qy	308	-----	307	Qy	308	-----	307
Db	103778	AGGCAAAACCATAAGGCCAATGATTTTAAACCAGGAGGTATATAGAACCCTCGGGAGC	103719	Db	102698	GGATTCAGGATGACCAGAGCTAGCCCTACTTTCAAAGGTTACAAACGCTACACTCAC	102639
Qy	308	-----	307	Qy	308	-----	307
Db	103718	AAGCAGTTTCAGGNAATGGAGAAAACCAAGATGAAAGCCTACCCAGGTCAGGCAATTG	103659	Db	102638	ATCCACGAATCACATATGGGCTATATGCTAAATTAGTACTTTAAACATTACTAATTTTAC	102579
Qy	308	-----	307	Qy	308	-----	307
Db	103658	AAGGGCTGTCAATCCCACCATGTCTCCCAGTAATCCCAAGTCTGTTCCAGGCAATTGC	103599	Db	102578	ATTTTACACCTTGCATTAGATTATCTGTCCCTTAAGTGTATTAACATGGGATATCTTAA	102519
Qy	308	-----	307	Qy	308	-----	307
Db	103598	TGAGGTGAGCAGGGTTGAGGAATTGCCCTCAGGCTCCCGGCTCCCGAGTGCAGGCTG	103539	Db	102518	GGAAAAAACCTATGGCATTTAAATGTAAGAATACTGTGATACTTCAATTAACCTAGTT	102459
Qy	308	-----	307	Qy	308	-----	307
Db	103538	AGGGTCTAATTTTCCCGGCTGTGGAGTCTGCCACCGGATTCGCCCCCTAGCCCGA	103479	Db	102458	TGAAAGTCTAGTTAAAAGTCTTCTTTTCAACATAAAATACTAAAAATACATACATACC	102399
Qy	308	-----	307	Qy	308	-----	307
Db	103478	GTCTGGCCAGGAGGCTTCAACCCGGTTCAAAATGTTACAAAGTCCAGCTGGAGACTTC	103419	Db	102398	CTGCACTAAATAACTTCATGTTAGTGAATTGGCACAATAACATTTAAAAGTTTATATA	102339
Qy	308	-----	307	Qy	308	-----	307
Db	103418	CTTCTCCCTGTGGCGTCTTCCGCCATGCTCTGGTGCCTCCAGAGGGTCCCTGTGGTTC	103359	Db	102338	GAAAGGATCTCACTATCTATTAACCTTCCTCTTTACAAAGGTAATTAATCATATGCTAAT	102279
Qy	308	-----	307	Qy	308	-----	307
Db	103358	CAGGCAGGAGTGGCTGTTGGGAGCCAGTGAGCTCCAGGGCCTTTCCCACTGTTTCTT	103299	Db	102278	GAAGCAGCTTTGGCAAGTGGTTACAAAAACATCAATAAATAAATAATGTTACATTT	102219
Qy	308	-----	307	Qy	308	-----	307
Db	103298	CTACCCATGTATTTGCTTGGCTCTCTAAATGACTCAGCTCCAGTAAGTTGGAAACT	103239	Db	102218	ATGGGTCACTGAAGAATGTATCTAAATTTAACATTTTAAATGACTCATAAAAATAAATGC	102159
Qy	308	-----	307	Qy	308	-----	307
Db	103238	TCTCTTGAGTATGACTTTTCATTTTCCAGTGGGGTGTGTGTCAGGAGTGGAGGTCT	103179	Db	102158	TGATCCTTACAAATGTATCTCATTTGTTATATTTTATTTTTCAGAAAAACAGAGTTCAC	102099
Qy	308	-----	307	Qy	308	-----	307
Db	102098	TGAATACAATTTCTCACTAGTTAAATCACAATTCACCTTAGTTAATTAATTTATGTTCA	102039	Db	102098	TGAATACAATTTCTCACTAGTTAAATCACAATTCACCTTAGTTAATTTATGTTCA	102039

QY	308	-----	307	QY	308	-----	307
Db	102038	AAAGATAGCTTTTCCTGCTATATAATTTCATTTTCTTAAAAAGCAAAACACTTTTCAGTAG	101979	Db	100958	GCCACCTTGGAGGCCAGCTGGGAGATAAAGCTGTAGGGATATAAAGGCTGTGCCAGGAC	100899
QY	308	-----	307	QY	308	-----	307
Db	101978	AAAAAATTTACATATAGAAAGTCAAAAACAATTTATTTTCAGAAAAAATGGAATCAACCACC	101919	Db	100898	CTTGGCCTGTGGCTGAGCCTCCACAATACCCTAGGAGTCGACCTTGCCTGTGTGTGT	100839
QY	308	-----	307	QY	308	-----	307
Db	101918	GTATCTTTCTTGGAGTTCTTCGACAGAACTATCCTTTCATCCTGACTTGTCTATGTGATT	101859	Db	100838	CAACAGTGGGAAGAGATTTCAGCAGAGAGCGAGGTATCCTCCTCTCGACTCTACCTCCTGT	100779
QY	308	-----	307	QY	308	-----	307
Db	101858	AAATAATGACGTGCAACTGAAAAAGAAAAAGAAATTCCTCATTTTAATCTCANNNNNN	101799	Db	100778	GAAGAATACGTNNNNNNNNNNNNNNNNNNNNNNCAAGTAGTTCATCAACATAACGAGAACA	100719
QY	308	-----	307	QY	308	-----	307
Db	101798	NNNNNNNNNNNATAATAGCATCATCAGCACTCCCATCCAGGAATATCTCACTCAGTA	101739	Db	100718	CACAGGGCGCTATCGCACAGAATAAAATTCGATGACTGGAAAAATTTTGTGTTAATTTTCAG	100659
QY	308	-----	307	QY	308	-----	307
Db	101738	ACAACTTCGAGAGTATCATGTCTACTACTTTTAAATACAGCTTCATATCCTCAGAACAAAT	101679	Db	100658	AGGTCCCTGAGCGCATATACCTTTTCAACTGAAAAAATTTGGGAGAAAAAGGAAGGTGAG	100599
QY	308	-----	307	QY	308	-----	307
Db	101678	TTCTATTTCCGCATCAAGATACTGAGTCACACGGAGACGCTTAATCTTTTCCCAACGTCT	101619	Db	100598	AGCGCCGGAACCGGCTTTTCATATAGAAATAGAGAGCGTTTCATGACTAAATGCTTGCATC	100539
QY	308	-----	307	QY	308	-----	307
Db	101618	ACCATAAATAGTAGTACGCCATACTCAGGCAGTCTAACTGCAGAGTCCATATTCCTAAA	101559	Db	100538	ACAATACTGAAGTTGACAAATATTATTAAAGGACCTATTGTTTTTCCAAATAGTGGTTA	100479
QY	308	-----	307	QY	308	-----	307
Db	101558	CACCATTTGACACTGCTACTCTCCCTGCCCGATTGTACTCTCAAACTTGACTCGTCAGT	101499	Db	100478	GCAATCGCTTACTTTCTTAACTTTTCTTACCTTTTACATTTTCAGCAATATATATATATAT	100419
QY	308	-----	307	QY	308	-----	307
Db	101498	CCTTACTATGCATGCCACAGAATATTCAAGGAATCTTGAATTCATTCAACAACATTTTA	101439	Db	100418	TTCAAGGATATACCATTCTAATGTCTGCCCTTAAGAGATCGTCGTTTTGCCAGGTGACC	100359
QY	308	-----	307	QY	308	-----	307
Db	101438	CTGTAGGTCCGGGAACCTTTGCTGTAACTGGAGAGCTCAAACTGAGCAGCAGACACTG	101379	Db	100358	ACGTTTGGTCAAGAAATCACAGCCGAAGCATTTAAGGTTCTTAAAGCTATTCTGTATGTTT	100299
QY	308	-----	307	QY	308	-----	307
Db	101378	TCCCAAACTTTCAGGGCCCCAGAGCCTATTGGAATTTATCTTTAATCTCCCTAATAACAATA	101319	Db	100298	GTTCCAAATGTCAGTTTCGATTTTCGAAAAATCATTTAATTGGTGGTGTCTGCTATCGACCTGC	100239
QY	308	-----	307	QY	308	-----	307
Db	101318	ATCTGATTGGCTCTCCCTCCCGACAGCAGTGTCTGGCATGAAGCTGATGCTTAAATGATTA	101259	Db	100238	AGGGGGGGGGGAAAGCCACGTTGTGTCTCAAAATCTCTGATGTTACATTTCCACAAAGAT	100179
QY	308	-----	307	QY	308	-----	307
Db	101258	CGGGTGGAAATGAAATGAACAGGAACAGTGGGCAGTCAGCTGGTGCCTGCTATGGGCCTG	101199	Db	100178	AAAAATATATCATCATGAACAATAAAACTGTCTGCTTACATAAACAGTAATAACAAGGGGT	100119
QY	308	-----	307	QY	308	-----	307
Db	101198	TAGCCTCAGAGGGTGGGAAGGAGAGAGCTAGTTTCCAGTTCAATTTCAAGGCCTTTC	101139	Db	100118	GTATTAGCCCATATTCAACGGGAAACGCTTTGCTCGAGGCCCGGATTTAAATTTCCAACATG	100059
QY	308	-----	307	QY	308	-----	307
Db	101138	ATGCCATCTCTCCCTCCTTCCCTGGCTGCCCTTCTGCTCCTACTCATGTCTCCTCTATCC	101079	Db	100058	GATGCTGATTTATATGGGTATAAATGGGCTCCGATAAATGTCGGGCAATCAGGTGGACA	99999
QY	308	-----	307	QY	308	-----	307
Db	101078	TGTGCTGACGCTTTGTTCAAAAGCTCAGCGTGACATTTTGAGGGTGATTGGTGGGATG	101019	Db	99998	ATCTATCGATTGATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAACATGCCAAAGGT	99939
QY	308	-----	307	QY	308	-----	307
Db	101018	GAGAGAGGAGGATGGAGGAAAAATTTCAATAAGGCCTCCCATGGGACTGCGAGCAAAATG	100959	Db	99938	AGCGTTGCCAATGATGTTTACAGATGAGATGGTTCAGACTAAACTGGCTGACGGAATTTATG	99879
				QY	308	-----	307

QY	339	-----	338	QY	339	-----	338
Db	97658	CCCACCTCCTACTACCATCACACTTGGGGGTAGTTTCAACTATGTTTTAGGGGCACAG	97599	Db	96578	ATGAAGCAATTTTGGAGCTGGTTGTTCACGCGGAACATGATCTTTTGTCTTTTAA	96519
QY	339	-----	338	QY	339	-----	338
Db	97598	GCCTTTAGACATTGCCAAGACATTAGTAGTGNNNNNNNNNNNNNNNNAGAACCCT	97539	Db	96518	CTGTGATTCTTATCTTATGGATGACTTGTNNNNNNNNNNNNNNNNNNHNCACATAGCT	96459
QY	339	-----	338	QY	339	-----	338
Db	97538	GAGTATCCACAGTTAATGCGGTCAAGATATTTCTTGAATCAGCGCCTTAGACCGTT	97479	Db	96458	TCATCATCACCTGCACCTTCTAAAGCCACTGTCTCTGCCCCCAGGACGACAAATATC	96399
QY	339	-----	338	QY	339	-----	338
Db	97478	CGCCCAACAACCAATTACTTCTTGAGAAATAGATATATTTACCCATATAATATAACGT	97419	Db	96398	CAGAGTTGCTCTCTTCCCTAAGGCTGGAATATGCCAACGCCCTGGCCACCCTTACACA	96339
QY	339	-----	338	QY	339	-----	338
Db	97418	TTTTGAACACACATGAACAAGGAAGTACAGGACAATTGATTTTGAAGAGAATGTGGATTT	97359	Db	96338	TTAAGCCCCCAAGTTCCACCTTCCCTCCCAACAACAGAGGCTGAGGCTGGTGCCTCCAGG	96279
QY	339	-----	338	QY	339	-----	338
Db	97358	TCATGTAATTTGGGATTCATTTTATAAGGCAATAATATTAGGTATGATATATAC	97299	Db	96278	CCCACCTCATGCTCTCCACACTGCCTCTCCACCACTAGGGCCACAGGCAGAGCTGTGTTTC	96219
QY	339	-----	338	QY	339	-----	338
Db	97298	TAGAAGTTCTCTCGACGCTCTCCCTTATGCGACTCCTCGCATTAGGAAGCACCCAGTAG	97239	Db	96218	TGGTAAGATGCACATCTCATCCATGGTTGGGAGGCACAACTTCTCTTCCAGGGGTTTT	96159
QY	339	-----	338	QY	339	-----	338
Db	97238	TAGTTGAGCGGTTTGAACCGCGCGCCGCAAGGAATGGTGATGCAAGGAGATGGCGCC	97179	Db	96158	CCACTTAGAAATCCCATAGGGTCTCTTTCCACAACCAGTTGGAAATGACCCCAAGCG	96099
QY	339	-----	338	QY	339	-----	338
Db	97178	CAACAGTCCCCGGCCACGGGECCTGCCACCATACCCAGCGCAACAAGCGCTCATGAG	97119	Db	96098	GAAGTTTCTCCCAAGAAAATTTATAGTCATAATCATAGGGAATTTCCAGATTCTACTGAGAT	96039
QY	339	-----	338	QY	339	-----	338
Db	97118	CCCGAAGTGGCGAGCCGATCTTCCCATCGGTGATGTCGGCGATATAGGCCCCAGCAC	97059	Db	96038	CTCACTTTGCCACAGGTGCTTCTCATACATTTATTTCAATTAATCTTTCCACAGTCTTAC	95979
QY	339	-----	338	QY	339	-----	338
Db	97058	CCCACCTGTGGCCCGGTGATCCGCGCCACGATGGTCCGGGTAGAGGATCTACAACCTC	96999	Db	95978	ACAGAGCAACCCAGTGGAAAGATTCTTCTCTGTGGCAGAGGAGGATTCTCCCCACA	95919
QY	339	-----	338	QY	339	-----	338
Db	96998	CACTTATTGTTAGGTAGAATTCCTCGTTAGTTGTTTATTAATTGCAATAATGGGGCGTCC	96939	Db	95918	CTCCTCAGCTCAGCCCCCTCCCTTGGCACTCTCCACCCCACTAGCTACCAATPAA	95859
QY	339	-----	338	QY	339	-----	338
Db	96938	AGTTTTGCAACAGTCTCTCTTACCAGGACACCTATGAGTTTGCTCATGGCAAACTAG	96879	Db	95858	CCCATCAGCACCAGCATTTTGCACAGTTTACTAAACAGGAACATGGTCTGTCTCTGCTGCC	95799
QY	339	-----	338	QY	339	-----	338
Db	96878	AGTGTTGAAAGTATGCATGGTTATAATTAGACAAATTCATTACCTCTGAAATCCTGCGC	96819	Db	95798	AGTCCCATCCCTGGACCTCTCAACTGTGGCCAGGTCCCTTCTGTATTCTCAATTC	95739
QY	339	-----	338	QY	339	-----	338
Db	96818	GTATACCCCATTTGCTGTTATCTTATTTTGGCTAAACCGCATTAAGAGCTTCGTTTA	96759	Db	95738	TCCTAACACTGCAACAGAGATCCATTCTCTGACCCCTGTACAGCCCCAGATAGGACGAG	95679
QY	339	-----	338	QY	339	-----	338
Db	96758	CCGTATGCAATGCGGTAGTTATCGAAGTTTGATATCCCGCAATATCAGCGGAACGCT	96699	Db	95678	GCCCCCTCTGTGTCMAAGGTCTTTTCAGTTTCTTCCCTTAAGCTTGCCCCACTCTTAAGGC	95619
QY	339	-----	338	QY	339	-----	338
Db	96698	TGTTCTCAGTAAGCATATTTCCGCGCAGCGCCTCTACTTTCTGCTTGAACCTCATGTT	96639	Db	95618	TCTACCCAAAGTAACATCACACCTTAAACAACCTCACCTGTCCACGAGCAGTGGGAAGAG	95559
QY	339	-----	338	QY	339	-----	338
Db	96638	TTTGATGCGTTTTTTGGATAACCGCAGATGTGACGCTTTGCTTTTGCTTTAGCGATCC	96579	Db	95558	TGACCAAGGCGCAGCCAGGCCACTCAGACCCCATGGACCCCATAGCCCTAGCTTTATTTCCCTTA	95499
				QY	339	-----	338

Db	95498	CAGTGGCCCCAGACAAACAAATCTTTGGGGAGATCAAAAAGTCAGGCTGGACTAAGGGATAT	95439	Db	94418	TGAGAGCCCAACAAACCCAGGCTCCAGCACACAGCCCCCTTCCTGGTATTAATTCGACTTGGGA	94359
QY	339	-----	338	QY	445	-----	444
Db	95438	TTGGGGCTGATCCTCCAAGGTGTCAGAAGGGAATTNNNNNNNNNNNNNNNNNNATTG	95379	Db	94358	GAGGGCACATTAGGAGGGGTGGTCTGGACCGTGGCCAGGTTGGTCAATTTCCTGTCTATC	94299
QY	339	-----	338	QY	445	-----	444
Db	95378	GCCTGGAAGTGAATAAGGCTTTGTGGAACCAAGATTGGGTGAGAAACCCGCAATTTTACA	95319	Db	94298	CCCAGGGGATTGATGATNNNNNNNNNNNNNNNNNNNNNTACAACACCCTAAGAATGTCT	94239
QY	339	-----	338	QY	445	-----	444
Db	95318	TGGAACACTGCTTAGTAAAGATTCCCTGCCCTATGGTAACAAGCCATTTGGAACCCCG	95259	Db	94238	ATAACCTCACTGACAGAACAGAACTAGCATGAGAGGTTCAAGTCACCCAGCCAGTAGCAA	94179
QY	339	-----	338	QY	445	-----	444
Db	95258	GGCCTGTACGCCCTGGNAATAATGGCCATGAAGCCCTCACGACCCTTCTCTTCCTACCA	95199	Db	94178	GTCCAGCTGGAATTTGNAACCTGGACCCACCCGAGCTGCAGTTTCCAAAACCCACTTGTTC	94119
QY	339	-----	338	QY	445	-----	444
Db	95198	CCTGAGAATCTGGGTTTGTGGACATCTCTGGACAGGATGCTCTACCATCTACGAGCCCT	95139	Db	94118	AGCCACAACCTGGGTCTCTGAGTGGGAAGGTCTCTCAGAGATCCCCCTGGTCCAACATCCT	94059
QY	339	-----	338	QY	445	-----	444
Db	95138	CTCAAAGGGCTCACTTTACAGTTTACAAGCACTTTACAGTTTACAAGCACAATCGCCC	95079	Db	94058	CATCTACAGAGGAAGAACTGACTTGGGGGGGTTTGGGAGTGTGAGGGATCCAGGTCAC	93999
QY	339	-----	338	QY	445	-----	444
Db	95078	CCTTGATTTCATTGGATCTCATGTAAATAGGATCAGATGTAAATAGGCAGACAGGCA	95019	Db	93998	ACAGTCAGTCCGTGGCAGTCAGCGCCAGGGGCTTCGGGCCAGCCAGGTTCCCTTCCTC	93939
QY	339	-----	338	QY	445	-----	444
Db	95018	TTGTCTGTCTCTGTCACCTTACAAGGAATAAAGCCTGGAGGTGAGGTACCTTGTCTAA	94959	Db	93938	CACAACAGGTAAGGATGCCCCCAGAGATCAATCTGAGAAACCGTGAAATCTGAGTCCTG	93879
QY	339	-----	338	QY	445	-----	444
Db	94958	CTCAGTTGCGCATACTTCGGACAGCAGACAGCTGTGGAGAGTTCAAAGTTCCACCCAG	94899	Db	93878	TGTGAGGCTTGGGTCACTGGGTGCAGGGATTCGACTCACGGCTTTCGAAGTGCCACAG	93819
QY	339	-----	338	QY	445	-----	444
Db	94898	AAGTGCTCCCATTTCTCAGTCTCCCTACACCCACCCACCTGCCCCCTTCTCTCCCTCA	94839	Db	93818	TGAGCAGGGGCTCAGGCCCCCGCTGGGAGAGAGGGCCACAGCTTCGGCCCACTCCTCCT	93759
QY	339	-----	352	QY	445	-----	444
Db	94838	CCAGCCACCTCTCTCCTAGCTTCCCATCTGGCTTCAGGTCCCTGAAAAGGACCTGTCTGG	94779	Db	93758	CCATCTCATGAGTTCTCAGGGGCTCGGGCTCGGGCCCGGGGAACCGTAGAATTTGGCAT	93699
QY	353	GGTTTCCATGAACATGCTCCTGCTGTGGCTGGGACAGGCCACCTGACACAGTATCGGA	94719	QY	445	-----	444
Db	94778	GAGTTGCAGTACAAACCACTGCTGTGCTGGCAGGGCCCTGGGCAGGCAATCTTAGTGC	94719	Db	93698	CTCGGTCTTGGAAGGCCCAAGTCGTGTTTCACTGGGGGGCAGAGGCCCGTAGGGGAG	93639
QY	413	G-----	413	QY	445	-----	444
Db	94718	GTCCCCAAGCAGAGGCTGAGGTCTGGCATGTGCAGGGGCTGGCCCCAGGGCTGGCGGA	94659	Db	93638	GAGAGAAATTTGAGGCTATGTGGGTATGAAACCCCACTGGGATGCCACCCCTCAGCACTC	93579
QY	414	-----	413	QY	445	-----	444
Db	94658	AGTCACTAGTGTCCCAAGGTATCCCTGCCCCGGTCACTGGGGCCCGCCAGTGCAGA	94599	Db	93578	CCCAAGTGTGCTGCTTCCAGGACTGCCCTGTCTGTCTGCCCTCCTGCCCCAGCCAG	93519
QY	414	-----	425	QY	445	-----	444
Db	94598	CACAGAGCCCTGGAGACTTAACGACAGGAATGAGAAGGAGGAGGAGCCAGGGGAGGAG	94539	Db	93518	CCCGGGCACCCCAACCTGGGCTCGGGCTCACCATGGCAGAGGGCACCTTCATCCAGCAG	93459
QY	426	AAGGACGAGGAGGATTC-----	444	QY	445	-----	444
Db	94538	GAAGGCAGGAATGCTTACCACGACGCCCTGTGTGCGAACAACAGTGCCTGAGTGT	94479	Db	93458	CACCTGGCAGATTTCCACAACTTGGCTCCGGGAATGACCCCAAGTCCAGGGGCCAAGAT	93399
QY	445	-----	444	QY	445	-----	444
Db	94478	AATGACTTGTGTTTATATAAAATGCCAGGTGGCCCCAGTCCCTGTCCTCCCAAACTCCCAT	94419	Db	93398	CCCATCCACCAAGTCCCGGCAGAGCAGCAGTGCCTATGGAAGGTAGAAAGGGGACAGGCC	93339
QY	445	-----	444	QY	445	-----	444
Db	93338	AGTGAAGAGGGGTGGCAGGGAGAGGAAGAACTATGCAATTAGATAGNGCACCTCTGAGG	93279	Db	93338	AGTGAAGAGGGGTGGCAGGGAGAGGAAGAACTATGCAATTAGATAGNGCACCTCTGAGG	93279

QY	445	-----	444	QY	481	-----	480
Db	93278	CCCAAGCCTGTTTCGTCGTGCTAGGATGCAGGTTAGGCCCGGCTTACATTAAGT	93219	Db	92198	TCCAGTCTGTGGTACTTTGTTATGTTAGCCCTAGCAACCGAGTACAGATGGTACTTACAT	92139
QY	445	-----	444	QY	481	-----	480
Db	93218	TGACGGAGAGGAAGCAATGAGGCTTGCGAAGAGCAACAGGGCTCAATTACGGTTGAGCTT	93159	Db	92138	TCTAGAACTCTTGAGAGGCTCTGACTAGGGAACACTAGGTATAGTAAAGGGTGATAGT	92079
QY	445	-----	444	QY	481	-----	480
Db	93158	AAGTGNNNNNNNNNNNNNNNNTATCCCGAAGAGCTGCCATGTATAATAGTGTGC	93099	Db	92078	CTGTTGGTAAATATACAGCTGATATTTGGGAAAAATCTCAGTCATTGTTGCTTCAACTA	92019
QY	471	CTTTGGGCAT	480	QY	481	-----	480
Db	93098	CATTCTGAATTTTCATGATGTATCCATTGGTCCACTACATTAAACCAATAAACTGAATCT	93039	Db	92018	TCTCTTGATGAACCACTCGNNNNNNNNNNNNNNNNNNNNNAATATCTAATTTCCAGCGAGAA	91959
QY	481	-----	480	QY	481	-----	480
Db	93038	GAATTTGTAGGAGTGGGTCAATATATAAATTCATAAAAAATTAATTTTATCAATCA	92979	Db	91958	CCTGTGTCCAGTAGCGATATGTCTACTCTAGTAAATCTGTGATCCGCATAGTTAAACAAGT	91899
QY	481	-----	480	QY	481	-----	480
Db	92978	AATAATGAATATTTAATAATACTGGGCATTGGTGTAAACAGAAAAATTTTAAAGCCA	92919	Db	91898	ATACACTCCGTATCCCTAACGTGACTGGGTCAATGTGCCGCCGACACCCGCCCAACACCG	91839
QY	481	-----	480	QY	481	-----	480
Db	92918	TCATTTGCTTAAACCTGTAAGTGGGTCAATAGGCTAATAAAAAAGAAACAGACAAATA	92859	Db	91838	CTGACCCNGCCTTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAAGCTGTGACCG	91779
QY	481	-----	480	QY	481	-----	480
Db	92858	TCTGTTAAATGAATTAAGAAATFAGGATAAAGGAGAGATTACTGTGCTTAAACATCAGCA	92799	Db	91778	TCTCCGGAGCTGCATGTCTCAGAGGTTTTCACCGTCATCACCGAAACGCGGAGGACGC	91719
QY	481	-----	480	QY	481	-----	480
Db	92798	AGAAGACTCTTAGTGGAGGTGATPACTTAAAGTTTGGGGGACTCCTAGGAAAGAT	92739	Db	91718	TGCGGTAAGCTCATACAGCGTGGTGGTGAAGCGATTACAGATGCTCGCTGTTTCATCCG	91659
QY	481	-----	480	QY	481	-----	480
Db	92738	GGTGATTAAACCACATTTTCTTCTTACCTTTCCTCAGATTCTAGTAAATAATAGTAA	92679	Db	91658	CGTCCAGCTCGTTGAGTTTCTCCAGAAGGTTAATGCTGGGCTTCTGATAAAGCGGCCA	91599
QY	481	-----	480	QY	481	-----	480
Db	92678	AGAATTACAAATGAATAATCATAAACAGCAAAAAAGAGGGAAGTGCATTAGGAACAA	92619	Db	91598	TGTTAAGGCGGTTTTTCTGTTGGTCACTGATGCCCTCCGTGTAGGGGATTTCTGT	91539
QY	481	-----	480	QY	481	-----	480
Db	92618	AAACTATTAAATACATTTTAGAAAGATGAAGGTGGAGGAGTTACAGAAAGGATTTGCATG	92559	Db	91538	TCATGGGGTAAATGATACGGATGAACAGAGAGAGGATGCTACGATACGGGTTACTGATG	91479
QY	481	-----	480	QY	481	-----	480
Db	92558	AGGGAGCATGAGAAAGTATTATGGCTAAATTATGTTCTCCTCAANTTCATATGCTGAA	92499	Db	91478	ATGAACATGCCCGGTTACTGGAAACCTTGTGAGGGTTAAACAACCTGGCGGTATCGATCCGC	91419
QY	481	-----	480	QY	481	-----	480
Db	92498	GTCCACCCCGCAGTACCTCAGAATGTGACTACATTTGGAGATAGGATCTTTAAAGAGGT	92439	Db	91418	GGGACCAGAGAAAAATCACTCAGGTCATGCGCAGCGTTCTGTTAATACAGATGTAGGTG	91359
QY	481	-----	480	QY	481	-----	480
Db	92438	AATCAAGTTAAAGTCAGGTCAATTAGGGTAGGCCCTAATACGATATGATTGCTGCCCTCAT	92379	Db	91358	TTCCACAGGGTAGCCAGCAGCATCCTGCGATCGAGATCCGGAACATAATGTTGCAGGCGG	91299
QY	481	-----	480	QY	481	-----	480
Db	92378	ATGAAGCGGATTAGGACACAGGCACATAGGGAGGGAAGACCATGTGAAGACACAGGGAGA	92319	Db	91298	CTGACTTCGCGGTTTCCAGACTTTACGAAACAGGAAACCGAAGACCATTTCATGTTGTTG	91239
QY	481	-----	480	QY	481	-----	480
Db	92318	AGACAGCCATCTGCAAGCCAAGGAGAGGCGCTTTAGAAGAAACCAATCCTACTGGCACC	92259	Db	91238	CTCAGGTCGACAGCGTTTTCGACAGCAGTCGCTTCACGTTCCGCTGATCGGTGATT	91179
QY	481	-----	480	QY	481	-----	480
Db	92258	TTGATCTGGACTTCTAACCTCCAGAATTGTGAGAAAAATAAATTTTATTATTAAATCCA	92199	Db	91178	CATTCTGCTAACAGTAAGGCAACCCCGCCAGCCTAGCCGGGTCTCAACGACAGAGCA	91119
				QY	481	-----	480

Db	91118	CGATCATGCGACCCGTGGCCAGGACCCAAACGCTGCCGAGATGCGCGGTGGCTGC	91059
Qy	481	-----	480
Db	91058	TGGAGATGGCGGCGCATGGATATGTTCTGCCAAGGTTGGTTGGCGCATTCACAGTTC	90999
Qy	481	-----	480
Db	90998	TCCGCAAGAATTGATTGGCTCCAATCTTGGAGTGGTGAAATCCGTTAGCGAGGTGCGGCC	90939
Qy	481	-----	480
Db	90938	GGCTTCCATTAGGTGAGGTGGCCGGCTCCATGTCACCGCAGCAACGCGGGAGGCA	90879
Qy	481	-----	480
Db	90878	GACAAGTATAGCGGGCGCTACAATCCATGCCAACCCGNNNNNNNNNNNNNNNNNG	90819
Qy	481	-----	480
Db	90818	CCACTGATCATCAGCATAGTACCTAGCACAGACGTTTGCACATAGTTAGGTGCTCACTG	90759
Qy	481	-----	480
Db	90758	ATACTATAAAATTTAATTGAATTTGACGCAAGAATCATATTAAAGTAAATGTTTAAAGTA	90699
Qy	481	-----	480
Db	90698	GCAGCCTAGCAAAATTTTGGGCATGGTGAAGCACTGGTAAACCAGTTAATTTTAGAGA	90639
Qy	481	-----	480
Db	90638	CTATCAAGTTGTTAAAAATATTAGGACACCATCCTTTAATTGTTATCAGCATCAATAAG	90579
Qy	481	-----	480
Db	90578	ACAGTTCAAGTTTACAATTTTATACGATATTGTGGTTAAATTTTATGGCCATTATACATAT	90519
Qy	481	-----	480
Db	90518	TACTATTCATTGAATTTTGAAGTAATCATATAATTTATTACAAAGATAATTTCTTC	90459
Qy	481	-----	480
Db	90458	AGATTGCTGATATAAATTTATGAGATATGTTTGAATTTGGATAGTTTGAATGCTTTAAAA	90399
Qy	481	-----	480
Db	90398	TACACTTGATAGATTTATAACTTTTATTGCTAAATGTATTATGATATATACACAG	90339
Qy	481	-----	480
Db	90338	GCAATTTGAATTTAGCTTTTATCTGCTATGATCTGAATGTTTATATATCCCCACAAATTC	90279
Qy	481	-----	480
Db	90278	TATGTTTAAATCCTAACCCCTGAAGCGCATGGTCTTCGGAGTGGGCCCTTTGGGAAGTAT	90219
Qy	481	-----	480
Db	90218	TGGGTCAAGAGGCGAGGCCCTTGTAAGAGGCCCCAGAGAGCTTGTCCACCAATTTACAC	90159
Qy	481	-----	480
Db	90158	CATGTAAGCACACATAAGAAGCACCATCTACGAACAAGAAGTGGGCCCTTCACACAGA	90099
Qy	481	-----	480
Db	90098	CCAGAGACCAGAATCTACTGGCATCTTCATCTTGGACTCCCCATCCTCCAGAACCTGAAG	90039
Qy	481	-----	480
Db	90038	AAATAAAATTTCTGTGTTTATTATTAAGCTACCCAGTTTGATATTTTATATAGCAACC	89979
Qy	481	-----	480
Db	89978	CGAATGGACTACGGTATGATCCTTTGAAGAAACTTACAAGTAGTCAGGCGAGGTAATGT	89919
Qy	481	-----	480
Db	89918	TATTGTCAATCTTAACATAAAGAAAGGAGGCTCAGAGGGTTAATGTTCTCTGTCATGATTA	89859
Qy	481	-----	480
Db	89858	TAGAGCTAAAAATTTGGCCAAAACAGTTTCAGAAAGTGTCTCTCTCTTAATGTAGAGCTA	89799
Qy	481	-----	480
Db	89798	TTTGAATCTACTTCCAGCTGCAGTTTATGTTGTGTTACCTGTGTAGAGACTGTTAACTG	89739
Qy	481	-----	480
Db	89738	AAGAAGTACAGATCACAAAGATTTACTATAGAATTTGAATTTTAAAAAATTTCTCATGTTT	89679
Qy	481	-----	480
Db	89678	GATGAACACGNN	89619
Qy	481	-----	480
Db	89618	AACTGAGAAACCCCTAGGCACTGCAAAACCAATTGAGTGTGGATTTCAGTGGTGTACAGACT	89559
Qy	481	-----	480
Db	89558	GAATGATGCCATACCCAAAATCCATATGCTGAACCCCTAATCCCACTGTGATGGTAT	89499
Qy	481	-----	480
Db	89498	GTGGAGACGGGCCCTTTGGGAGGTAACCTGGGCCATGAGGTGGAGCCCTCATGCTGGAT	89439
Qy	481	-----	480
Db	89438	TACTACCCCTTATTAAGAAAGCAAGAAAGAGCTGCTTCTCCCAACCCCAACCCCGGTT	89379
Qy	481	-----	480
Db	89378	CTCTCTGGCTCTTTATCTGCTGCTCTGCTGCTGCCAGTGAGGATACAGTGAGACAA	89319
Qy	481	-----	480
Db	89318	CAGCCATCTGCAAAACCAAGGAGGGCCCTCACCAACACCAAGTCTGCTGGCTTCTTGA	89259
Qy	481	-----	480
Db	89258	TCATGCACTTATCAGTGTCCAGACTGTGAGAAATAAATGTTCTTGTGTTTAAGCCACCCA	89199
Qy	481	-----	480
Db	89198	GTGTATGGTATCTTAAATAGCTCTCTGAACTAAGAGACATGAAATAGTATGCTCT	89139
Qy	481	-----	480
Db	89138	GCCTATCAGTGGGATTAATAATGTGCAGTGTATTTTAAAGAGTTGATCTCCAAAGTACAG	89079
Qy	481	-----	480
Db	89078	TACTTAGCAGTAATATGAAGTTAATAATGTTTGTAGTAAAGAACGAATGCAGGCA	89019
Qy	481	-----	480
Db	89018	GTATAGAATGAGAATCAAGTATCCAGATGAAGCCTTAAAGTTTGGCTGAAAGCACTTGCT	88959
Qy	481	-----	480
Db	88958	GAACATTTAAAGACCTTTTCATCATCAATGAGGATTATTTAATGCCCTTTTATAGATT	88899

QY	481	-----	480	QY	481	-----	480
Db	88898	GTGTTACAGAGTCTCTCCCAAAATGTTTTTGAATACCAAAATGAATGATAAAAGGAAT	88839	Db	87818	GCTGCTGGCTTGGATATCACCCACCTTTTGACTTCATGTTAACTGCCTCATGCAGGCC	87759
QY	481	-----	480	QY	481	-----	480
Db	88838	AGGGTTATAATGTTCTGTTCTCATGTGAATCCCTGTTTCATGGCAGTTCAAAATAGAC	88779	Db	87758	ACCCTCTGCTACAGTCTCAGGGTCTCTGCCAGGTGTGAGCCTCCCTCATCATCCACCC	87699
QY	481	-----	480	QY	481	-----	480
Db	88778	TAATATTAAGCTAATATTTATATACATCCTACTGTGTGGCAGCAGCTTTACCAAGGGTTCT	88719	Db	87698	CCACCCAGACAGCTCTCAGCCACCTCCGGGATCCTGGAGTCAGCACCATGTTTCAGACA	87639
QY	481	-----	480	QY	481	-----	480
Db	88718	GCATATATTATCTCAATCCTAGAACATGCAGAAATAGTTTTCTGTGAAGCTGGGGTC	88659	Db	87638	GGTAGAGTCGCTGACTCTACTCCTCCCGCAATAAAGTCCAGGAATCGGGTGGCTG	87579
QY	481	-----	480	QY	481	-----	480
Db	88658	AAGCAGAAGCTAGTCTGACTTAGAGGCTCATATTCTCTCTACACTGCAGTGGTTGCT	88599	Db	87578	AGTCCACTTTTGGCTGGGAACAACCTTAGAGAAATCACAAAGGTTCAAGCGGAGTCTATC	87519
QY	481	-----	480	QY	481	-----	480
Db	88598	GAGCAGCTCAGGATAACAAAGACACAGCGGCTGGAGAGGAGCGCTGCAGCTGCC	88539	Db	87518	GGNAGATTGTGTTGAAGCCTCAGTAGAACCAATTTAGTCAACAAAAAATTTTGGCCACA	87459
QY	481	-----	480	QY	481	-----	480
Db	88538	ATTTCTCGGTATTACTACCACCTACTGGATCTCATGAAGAACTGCTGNNNNNNNNN	88479	Db	87458	TTCTTGGATGAGTTTGTGTAATCTGAGATCCTTCCAATTCAGAGCTGCTTTGTCTAGGG	87399
QY	481	-----	480	QY	481	-----	480
Db	88478	NNNNNNNAGATCGATCATCAATATCCAGTTGGGAGGGTTTCTGTGATTGGCCAGGCTG	88419	Db	87398	TGGCTGTCGGGCTCTCGTCTGTAATTTCTGTCAAGCTGCTCTCTTAGAATTTGACATG	87339
QY	481	-----	480	QY	481	-----	480
Db	88418	AGGTAGAACAGCTCTTCCAAAACATGAGGTGGAAGAAAGTGACCTGATGTGACTTT	88359	Db	87338	TTTTTAGAAATTTAAAGGCACAGAGTATCTTTGAGAAATTTNNNNNNNNNNNNNNNN	87279
QY	481	-----	480	QY	481	-----	480
Db	88358	CAAGAGTACCCGAAGTGCCCTCGCTCCTGAACCCAGCCCTGCTGTCTGCCCTGG	88299	Db	87278	ATATATGAGAGACCCACATATGTATATCAAAACTTATTTACTCACACTGCGAAACAGAGAA	87219
QY	481	-----	480	QY	481	-----	480
Db	88298	CCTGTCTAGAGTCTCTGGAGGGTCTGCTGCCTGTGTTTGGGCTCTCAGTGGGCTCC	88239	Db	87218	TTATTTCTAAACCCCTTAGAAAAATATACCACATATAACTCTAGCGCCAAAGTCTTACAGG	87159
QY	481	-----	480	QY	481	-----	480
Db	88238	CCTCTGCCCTCCCCAGACTCTTCACTTATGTCAATGAGAAGCTGTCTCCAAGCCACCT	88179	Db	87158	GCTCTACAACTAAGAGGCACACGGCGGAGGAAATATATAACATCCACCATATTTACAAA	87099
QY	481	-----	480	QY	481	-----	480
Db	88178	ATGCAGCCTTTCATCAACCTCTCAACAACTACCAGGGGCAACAGGCCATGGGAGCACT	88119	Db	87098	GGCAGACACAGGCACAAAAATTTGCCTGAGAACAGAGAAATTTGTGAGGTAAACACAACAC	87039
QY	481	-----	480	QY	481	-----	480
Db	88118	TCAGTCCCGAGGAGTGGCCGAGCAGGAGCGCTTCTCTCAGAGAGATCATGAAGACAGCAG	88059	Db	87038	ACGGGAATATTGCCCATATACCAAGGAGCGCTTTCTTAGAACATGGAACGCCACCTTA	86979
QY	481	-----	480	QY	481	-----	480
Db	88058	TCATGAAGAGCTCTACAGCTTCTCCATCACACAGAGTGAGTGACACCCCGAGCCCCA	87999	Db	86978	AACACACTGGTGAACAGGAACACCAACCCAGGTTACCAGGCCCAACTGCAAAAAGACAAAG	86919
QY	481	-----	480	QY	481	-----	480
Db	87998	GAGCCATCAGTCTCTCAGCGAAGCCAGGTGGGGGGGAGGGAAGTTTAGGAGGC	87939	Db	86918	GCCAAAAATTTGCTAAAAAGCCCATTTGGATGCTTTAGGAAGAAACTTTGCATCCAATTAACA	86859
QY	481	-----	480	QY	481	-----	480
Db	87938	AGGTGAGGAGGGTGGGACTCTCTGGAGGTCACTGTACATCTGGAGGGATGAGGAT	87879	Db	86858	AGTCAAAAAATTAAACAGCGCAACATCCATAATGCCAGGATCAAAATTTCAACACCAACA	86799
QY	481	-----	480	QY	481	-----	480
Db	87878	GAGGCCAGGGGAAGCCAAAGAGAGGTTAGGAACCAACCAAGGAGCTGGCACATCCTCTG	87819	Db	86798	ATATTACCTTTAAATGTAATGGGCTAAATGCCCAATTTAAACACAAAGACTGCAAAAT	86739
				QY	481	-----	480

Db	86738	GGATAGAGTAAGACCATCAGTGTGCTGCTGCTAGGAGACCCATCTCACGTGCAAGAC	86679	Db	85658	GAGCCCTCAATCGATATGTTATATAGTCTCTCGGTGTTATCCACACATATAGTCCTCTA	85599
Qy	481	-----	480	Qy	526	-----	525
Db	86678	GCACATAGGCTCAAAATAAAGGCATGGAGGAAGATCTAACAAAGCAAA	86619	Db	85598	CTAAGGAAAAATAAAAAATGTGCTAGTCCACGATTCTCAATCTCTTTTGACTCACACT	85539
Qy	481	-----	480	Qy	526	-----	525
Db	86618	AAAGCAGGGGTTGCAATCCAGTCTCTGATAAAACAGATGTTAAACCAACAAAGATCAA	86559	Db	85538	ACTTTCATGGTAATAATAATTTTCATAGACCTCCACCAGAAATTTTCCTCTATTTTTAT	85479
Qy	481	-----	480	Qy	526	-----	525
Db	86558	AGAGACAAAGAACCCACTACCTAATGTTAAAGGATCAATTCACAAAGAAGATCTAACT	86499	Db	85478	ATGATAAAACAATGATTTTATAGTAAGATTTTATTTTATTTTATTTTATTTTGAGACAGCATCT	85419
Qy	481	-----	480	Qy	526	-----	525
Db	86498	ATCCTAAATATATATGACCCCATACAGGAGCACTCAGATTCATAAAGCAAGTCCCTAGA	86439	Db	85418	GGCTCTGTTGCCCTAGGCTGGAGTGCAGTAGTGTGATGTCTAGCTTACTGCAACCTCCATCT	85359
Qy	481	-----	480	Qy	526	-----	525
Db	86438	GACCTACAAAGAGACTTAGACTCCCAACAATAATAATGGGAGACTTTTAACACCCCACTG	86379	Db	85358	CCCGGCTCCAGCCATCTTCCCACCTCGCTCTCCCAAGTAACCTGGGACTATAGCATGCA	85299
Qy	481	-----	480	Qy	526	-----	525
Db	86378	TCAATATTGGACAGATCAACGAGACAGAAAGTTTAAACAAGGATATCCAGGACCTGAATCA	86319	Db	85298	CCACCATGCGCAGCTAATTTTTTATTTTGTAGAGACGGGCTTTTGCCATGTTGCCCA	85239
Qy	481	-----	480	Qy	526	-----	525
Db	86318	GCTCTGCAACAACGACACCTAATAGACATCTACAGAACTCTCCACCTAAATCAACAGAA	86259	Db	85238	GGCTGCTGGATCCTTAAGCCCAAGCAATCTGCCGCTCAGCCTCCCAAGTGTGGGA	85179
Qy	481	-----	480	Qy	526	-----	525
Db	86258	TATACATTCTCTCAGCACCATCACACTTATTCAAAATTTGACCACACAATTTGGAAT	86199	Db	85178	TTACAGCGTAAGCCACCGTGACGACCATTTAGATTCATTAAAGCACATTTAAATACAAA	85119
Qy	481	-----	480	Qy	526	-----	574
Db	86198	AAAGCACTCCTCAGCAATGTGAAGAACAAGAAATCACACAACCTGTCTCTCAGACCAC	86139	Db	85118	CTTTAATTAATATGATAACAAAATCTTTTGTGATTCAAAACACTAAAGTTATTACGTAG	85059
Qy	481	-----	480	Qy	575	TCAGAATAATGCCT	588
Db	86138	AGTGCAATCAATTAGAACTCAGGTTAGGAACTCACTCAAACTGCCAAGTCTNNNNNN	86079	Db	85058	GAATAAATTCCTTATAAAAAATAAAAAATATATGATAGTTTCATTAAATGAACATTGAA	84999
Qy	481	-----	480	Qy	589	-----	588
Db	86078	NNNNNNNNNAATAGATATTACGGAAAGATCATTTGTAAGAACAGGTCAACCAAAA	86019	Db	84998	ACATGGACTAAAATTTAGTATCTGTGTTTAGCATGAAGATTTAGAAATACCACAGCCT	84939
Qy	481	-----	480	Qy	589	-----	588
Db	86018	ATCTACTTGACCCATAAGCAAGCCACAGAGTGTCAATCAACCTTTAATCAGCACTATCA	85959	Db	84938	ACCAACATTCCTCCAGGATTTATCCAACCTGCTATGCTGACATGTATAGAAAACTAACA	84879
Qy	481	-----	480	Qy	589	-----	588
Db	85958	GCAGTAAGGCTTAGGCTTAAAGGAAGTTCAAAATACCGTAAACTAATAATAAAGCACCC	85899	Db	84878	GCAGCAGAACNNNNNNNNNNNNNNNNNNNGCTGATGCCGAGTTGCTGAGGCGCAACAT	84819
Qy	481	-----	525	Qy	589	-----	588
Db	85898	AGTAGCAGAAAAGTTTAAAAACAATGTTGCTTTCATTAGTTTAAACCAAAAAAAGTCT	85839	Db	84818	GACGCAAAAGAAATTTGAGATTTCTTCTCTTCTGAGCTGTGAGCAGAAGACCCAGA	84759
Qy	526	-----	525	Qy	589	-----	588
Db	85838	ATTTTAAACTGCTATTTTAAAGCAAAAAAAGAGACATTAATTAATCTTCACT	85779	Db	84758	GACCCCTAGGGTAAGGGAAGCAGCCACCCCTACAGTGCCTCCAGCAACAACAGCCAGCCAG	84699
Qy	526	-----	525	Qy	589	-----	588
Db	85778	AATAACCTATGAGGAAGGTATAATTACCATGTTTTTCACTTGAGGGAAGTGAATGCAG	85719	Db	84698	CCTCTCAGAGATCCAAAGCTGGATGGGTGGGGAAGCAGAGGCTCCAGGGGACCCAGGGA	84639
Qy	526	-----	525	Qy	589	-----	588
Db	85718	AAGTTAGTTAACTATTCAAGGTCACCTCAGCTAGTAGTAAGTGACCAAGCTCTACTTCTCCAA	85659	Db	84638	ACAAATAGGTGCGCAGATTGGCAACATACTAAGCAAAAGAGGGGGCTTAGGAAAAGGTA	84579
Qy	526	-----	525	Qy	589	-----	588
Db				Db	84578	GCCGGGGGACTCTGGCCACGCCCTACCCACTGGACAGGGACTCACTGGGCGCCGACGTT	84519

QY	589	-----	588	QY	589	-----	588
Db	84518	AATGAACCTCTGAGCAGCTGGCCCGGGGGCCGCGCAGACAGACAGCTCGGT	84459	Db	83438	ACATACTCTTGGAGTCTTAGGGCCCGCCACTGCTGTTCTCTCTCCATACACACAG	83379
QY	589	-----	588	QY	589	-----	588
Db	84458	GGCCACCAGTACTGACAGCTCATTTGAAGCGGCGCATGAAGCGCTCCAGGTTGGCGGTGT	84399	Db	83378	CTGATGCTCTCTGGAAAGCGCCACTACTTGGCAGGAAGGAACACAGACAAAAATAGAAC	83319
QY	589	-----	588	QY	589	-----	588
Db	84398	GACATCCCCAGATGCTGGGGGCCAGCACATAGTGGATCAGCTCCACCTGGGTGGGGTC	84339	Db	83318	ATTAAACCAACCAAGCTAAAGAACCTTCACAGAGTCCATTTC AACCCCTCGCGCTCCC	83259
QY	589	-----	588	QY	589	-----	588
Db	84338	AGCAGAGAGGTCAGCGAGTGTGAGCCGAGCGGGCCCGCCCTGCTCTCTCC	84279	Db	83258	ACAGCTGAGAGGCCCATAGATTACATCACAGGACTCTGTGCAGACAACCCCGAGTA	83199
QY	589	-----	588	QY	589	-----	588
Db	84278	CCAGCTCTGCCTCCCATACCTTGTGTGATACTGTGTAAGAGGCTCCAGTGTGTGCGTCA	84219	Db	83198	CCAACCCAGAGCCAGGTAGGCTTGTGTGTAGACCCAGAGAGAGATACCAATCACT	83139
QY	589	-----	588	QY	589	-----	626
Db	84218	GCTGGCCTCCAGGTCCTTTGGCACTCACAGGTCACAGCTCCAGCCCTCAGCAGAGCCACAGTGG	84159	Db	83138	GCAGCTCAGCTTACAGGAAGCCGTATCTATAGGAAGGAAGAGACTACTACATCAAGG	83079
QY	589	-----	588	QY	627	-----	626
Db	84158	GCCCCAGCTGGTCAGGGTGTGGGATCTGCGGGTGGGAGAGTGTCTAGGGGGCTGCTGAG	84099	Db	83078	AACACCCCATGGGACAAAAGAAATCTGAACAACAGCCTTCATCCTAGATTGTCCCTCTGA	83019
QY	589	-----	588	QY	627	-----	626
Db	84098	GAATCCAGGAAAGGCACAGGCTAGGGGAGAGGTTGGGCAAGGACTCTATGTCGTG	84039	Db	83018	CAGCCTTACCCGAATGAGAGGAAGAAACCAACTCTGTGAATATGAAAAAACAAGGCTC	82959
QY	589	-----	588	QY	627	-----	626
Db	84038	TTAGGAGGAGGTTAGGAGGCGCAGGAGTGGGAGTAGAGGCTCTTAGGGGTATAGCAG	83979	Db	82958	TTTAACACAGCAAGAAGAAATCCCTGATTTTACCTGAAAAGAAATTCAGCAGGTTAGTTAT	82899
QY	589	-----	588	QY	627	-----	626
Db	83978	CTGGAGATAGGCTCCCGAGTGTCTGAGACCCCTCTTTTGGGCTCCTCTCTCTGGGA	83919	Db	82898	TAAGCTAATCAGGGGGCAGCAGAAAAAGGCAAGCCAAATGCAAGGAAATCCAAAAGATA	82839
QY	589	-----	588	QY	627	-----	626
Db	83918	ACCCTTAAGGAGGCTCCTCTCTTTCTCTGGAGCTCCCAACCAAGTCTTACCAG	83859	Db	82838	CAAGAAGTGAAGGAGAAATATTC AAGGAAATAGATTAAATGAAAAAACAATCAAAATG	82779
QY	589	-----	588	QY	627	-----	626
Db	83858	CCCCTGCCCTGCACTATCTTTGGGAATTCCTCCCATCAGCTGAGGCCCACTCTTGTGTGC	83799	Db	82778	TCAGAAACATTTGGACACACTTACAGAAATGCAAAATGCTCTGGAAGTCTCAGCAATAA	82719
QY	589	-----	588	QY	627	-----	626
Db	83798	TGAGGACCCAGCAGCAGCAGAGCCAGGCCCTCTCTCCCTCTCTCTCCCTGGACCTCCC	83739	Db	82718	AATTGAACAAGTGAAGAAGAAATTCAGAGCTCAAAGACAAGGCTCTCGAATTAACCCA	82659
QY	589	-----	588	QY	627	-----	626
Db	83738	CAGAATCCACCAGTGCACACTCAAAATAGATCTCTCTCTGGCCCTGGCACCTGCT	83679	Db	82658	ATCCAATTAATAC	82599
QY	589	-----	588	QY	627	-----	626
Db	83678	GGTCCCTACCAGCTCATGACTTCTCTGTGNNNNNNNNNNNNNNNNNNNNNACTGCATGAC	83619	Db	82598	ATATGAACAAGCCCTCCAAGAAGTCTGGGATTTATGTTAAATGACCCACATCTAAGATAAT	82539
QY	589	-----	588	QY	627	-----	626
Db	83618	TCAGCAGAGTAGCTATAATACTCATAGGTTTCACAACCTCCATCCAGCTGATGGCTTCACCT	83559	Db	82538	CAGTGTCTCCTGAGGAAGAGAAGTCTAAAAGTTTGGAAATATATTTGGGGGAATAAT	82479
QY	589	-----	588	QY	627	-----	626
Db	83558	CCAGCCCCCAGCAGCAGCAGCAAGACTCCCTCTAAGGAGAGTCTGAGCTCAGACACTCC	83499	Db	82478	CAAGAAAAATTTTCCAGCCTTCTAGAGACCTTAGACATCCGAAATACATAGATTCTTAG	82419
QY	589	-----	588	QY	627	-----	626
Db	83498	TAGTCCACCCCACTGATGCTCTTCCCTATCCACCAGGATAGTGAAGACAAAGGAC	83439	Db	82418	ACAGATAATCACTCGGNN	82359
				QY	627	-----	626

Db	82358	AACAAAAAAGGCCACTACAAAATGTAAAAAGCGGATAACAGACACACAACAAATACAGGG	82299	Db	81278	CTCCCTCAGGCAAGAGCTTATGCCCGGTGTGTGTCGAGAGAAATGATGCCAGAGCCGC	81219
Qy	627	-----	626	Qy	627	-----	626
Db	82298	ACAGCACTATGGAAGCATAAAGGAATTAACACCAACACGAGAGTAATCACCAGGAAC	82239	Db	81218	GCGGATCTGCACCACCTGCCAAGCCACAAACCCTGGTGAGAGGGCGGTCCCTCGGGTG	81159
Qy	627	-----	626	Qy	627	-----	626
Db	82238	CAAAATGAACCCACCGGGTAACCAAACTGAGCCGACACAAAGACACATCCCAACATGTAA	82179	Db	81158	GGAGTCCCCCACCCTACATCCTCTGTGGAAGAACTATGTGNNNNNNNNNNNNNNNN	81099
Qy	627	-----	626	Qy	627	-----	626
Db	82178	CCCCACTTAAAGGCACCTAATACTACTTAAAGGTAACACAGGGATACATGAACACAACCA	82119	Db	81098	NAACCAACCATGTTTCCCCAACAGAGAATGGACAGTGTTCGTAAGCCAGGCCCCCAT	81039
Qy	627	-----	626	Qy	627	-----	626
Db	82118	TACAAATTCACCCCAATACCAGACTTCATCCACCCCATTACCACCATATCATGCATCAA	82059	Db	81038	GTTACCTCCACTAAGCCCAACACAGCAGAAGTGCCTTAACAATTTTAATGAAGGGAGCA	80979
Qy	627	-----	626	Qy	627	-----	626
Db	82058	TCCCAATCCCCATGCCAAAACCTGAGAGTGAACACAAAACCTGTTGGAGAGATCATACATA	81999	Db	80978	CATCTATTATCATAGCTATATACGTAAACTTAATAGTAGAAGATTTGAATTAGACAGAAA	80919
Qy	627	-----	626	Qy	627	-----	626
Db	81998	ATGCTGATGCATCAGGAAGTGCAGAGATGAATTAGAGTTCCTTAGACTGGAAGATGAA	81939	Db	80918	AGTCATTTGATATTAATAATGTGCAGAAAATCTAATATATATTGAGGATTNATGTTTAACTC	80859
Qy	627	-----	626	Qy	627	-----	626
Db	81938	GACATCCAGACAAATACGGCTGCCCTCAGGGCTAAGAGATACAGGAAATGCTGCTGG	81879	Db	80858	AAATATATATGCATCTCGCATTTACTCCGTTTTATTATTAGCTGCTGCTATGTCCTCAGG	80799
Qy	627	-----	626	Qy	627	-----	626
Db	81878	GGCTTGAGGGGAGAGGAGCGGGCTCTATGGGTGAGGTAGGCCCAAGGAGCCGTTA	81819	Db	80798	CTTTAGCATCAAAAAGAAAACATCATATCAAAAGGAAGCTGACATAGTATTAAAGTCAACA	80739
Qy	627	-----	626	Qy	627	-----	626
Db	81818	TGCCCTTCACCTTTCTCGGCTACAGGAGGCAAGATTTGGGACCTATGAACAAAC	81759	Db	80738	GAAGGAGCGAAAGCAAAATTTGAAGCACACAGAAATGAAGCAGCAGGCCATTTTCAGAGAAA	80679
Qy	627	-----	626	Qy	627	-----	626
Db	81758	CATCTCTTGCAGACATGACCTTCATTCATGAGGGAACACACACTAGTGGAGATCTC	81699	Db	80678	GATCGGTAATCCAAAGCTATTCACAGTACAATGTATATGTTTTGCTGAGTGTGATTT	80619
Qy	627	-----	626	Qy	627	-----	626
Db	81698	ATCAACTTTGAGAAGATGTTGAGTCCAGGAGAGCAGGCATTCACACTAAACATAGGTTG	81639	Db	80618	ATCTCTGTATATCAGTTAAATTTCTTCTCTCTAATATAAAGTTTTGCTGAGTAGGA	80559
Qy	627	-----	626	Qy	627	-----	626
Db	81638	GAGGACATGACTGTGGCCTGGGAAGGGCAGGGCTGGAGGCAGCTTAAACTTGTATGA	81579	Db	80558	ATTGGGAATTAATGCACTAAAGCCTCTGGACCTACTAATTCAAAATTTGGGTAATTGA	80499
Qy	627	-----	626	Qy	627	-----	626
Db	81578	ATAATATGAGGATCAATCTACTGTGTAATAGCCCTGCCTTATTCACACTGCACTGGG	81519	Db	80498	TGACTTTATATATAAATTAATAAATAAATAACTATAGAACAACCTTAAGTTTAGAAAACACTT	80439
Qy	627	-----	626	Qy	627	-----	626
Db	81518	TCTGCCAGGTGCCAGCCTCAGACGTCACCATTCACAGAGAGCCCTCCAGCCCTCTT	81459	Db	80438	TTGAATCTTTTATATATTTACATATACATAGTTATAAATTTAACATAGAAGTTAATPACA	80379
Qy	627	-----	626	Qy	627	-----	626
Db	81458	CTCTAAAGCCTTTCTCTCTCGCCTCTGCCTTCTGTCTCTGCTGCTGCTCCCGCTGGC	81399	Db	80378	ATCCATTTTATAATGTACTTTTTTCATTAATTACACTGGACTGTTTCTGATTTGAAAT	80319
Qy	627	-----	626	Qy	627	-----	626
Db	81398	CTCTGGGTGCTGAGCGGAAGTACACATGATGCCACATPAACCAAGATCTTACAGTCCC	81339	Db	80318	CCTCTACTAATCATGAGTTCAGGTTTAGTTTATTTATTGCTTTCCTGGACCCACAGAGG	80259
Qy	627	-----	626	Qy	627	-----	626
Db	81338	TGATCCTTGTGTTTCAGAGGAGCTTGGCCTCCCTGCTGCTGCACAGGCGCAGCAGGCTT	81279	Db	80258	ATTCCTAATAAATATTTATGAATGATTTATTGATTGATATTTGACTGATTATAACTAA	80199
Qy	627	-----	626	Qy	627	-----	626
Db	80198	ATGTTATAGTGAATCAGGTATACAAATTCCAATACAGCTGAATTTATCTATATTGTTGG	80139	Db	80198	ATGTTATAGTGAATCAGGTATACAAATTCCAATACAGCTGAATTTATCTATATTGTTGG	80139

QY	627	-----	626	QY	668	-----	667
Db	80138	CATATTAAAGTTATTGAAGAGTGGGCTTTATAAATCTGGTACTGATTTCTTTTCACAAAAT	80079	Db	79058	ATAAGCTGAAGAGCGATTATGACTTTATCCTCGTTGATAGTGGTCTCACCTTGACGCT	78999
QY	627	-----	626	QY	668	-----	667
Db	80078	TTATTTTGTGTAATGGAGGTCCTTTGTGTGACCAGCTTGCATATTTGTGACTTAAGGA	80019	Db	78998	TCCTGAAAAATGCTTTTGGCTCGGCCAATATACTGTTACACCTCTGCCGCCAGCAACTG	78939
QY	627	-----	626	QY	668	-----	667
Db	80018	CAGGTATTGATTAGTTGGGACCTTTTGGTTAACAGTTAGGGTGTCTGTAAAGATTATAA	79959	Db	78938	TCGATTTCCACTCATCGCTTAAATACGTTGCCCGCTTCTCTGAGTTGGTGAACATCATTT	78879
QY	627	-----	626	QY	668	-----	667
Db	79958	GGGCTTTGGTGTATATAGTGTGATATTAAGATGGAATGATATGAGTGTGGATATACT	79899	Db	78878	CGGATGAAGGCTGCGAGTGCAGCTTGCAGCTTAACATTTGGTTTATGTCCAAGTTGAGTA	78819
QY	627	-----	626	QY	668	-----	667
Db	79898	AGTCGAGAGTGATAGTGTAGTTAACACTGGTGTCTCTCGGCTTTGTAAAGGATCTTGT	79839	Db	78818	ACAAGGCAGACCATTAAGTATTGCCATAGCCTGGCTAAAGAAGTGTTCGGTGGGATATGC	78759
QY	627	-----	626	QY	668	-----	667
Db	79838	ATATAGGTTTATATGATGCCCATTTTGATGTGGGTGAGTATACTCCCAATTACTGAGGAG	79779	Db	78758	TTGATGTCTTCTCCCTCGCTTGACGGTTTGAACGCTGCGGGANGTCTTTTGACACACTG	78699
QY	627	-----	626	QY	668	-----	667
Db	79778	TTGTNNNNNNNNNNNNNCGTAGTTTCATCGACAAATGAGCAACAGAAATGCTC	79719	Db	78698	TATTTACAGTAACCCGGCAGCTATGTTGCTAGTCTGATGCATTTGAAGAACGCGCAATT	78639
QY	627	-----	626	QY	668	-----	667
Db	79718	AATGTTCTGACTGAACAAGTACAGTTGCAAAAGGATGAGTACACGCGAAACGAGTTTAC	79659	Db	78638	TGCGCGGAAGATTTTGTCTAAAGCAGTTTTTGACCCTATTTGAATTTATCAGATCTAACTGA	78579
QY	627	-----	626	QY	668	-----	667
Db	79658	CAGGTCTATGCGAAGCGCACTGGCAAAATTCCTCTACTGACTCGAGCGAAGTTGACT	79599	Db	78578	AGAGTAAGAAATCCCATGTCAAGAATCAGACCCACATTTGGCGACCTNNNTATCNTCAAT	78519
QY	627	-----	626	QY	668	-----	667
Db	79598	ATGCGGTAAAGTGAAGAAAGGTTATGTTTTCGATAAACGCCCTGCTGCTCTT	79539	Db	78518	ANTAAGCGGATTTTAAAGTTCTCCAGCTTCTTGGGATCCGAGTCCGGCAGGTATTCAC	78459
QY	627	-----	626	QY	668	-----	667
Db	79538	CAATGAAATATGCGATGTCAATTCAGAACATCATTTGACATATATGAACATCGCGAGTGC	79479	Db	78458	AGTTTAAACTGGGCGCCAAGCCACATTTTTTTGAAAGGGGAACCCCGCTTTNNNNNNNN	78399
QY	627	-----	626	QY	668	-----	667
Db	79478	CNAATACGGGGATCGCTACACCGAAGGAGTGTGATTTTCATCTCCAATCTTAAAGGG	79419	Db	78398	NNNNNNNNNNNNAACAGGGGCAATTTGAGTTACTTAAGAGCCTCTTAGGGGTAATACGTG	78339
QY	627	-----	626	QY	668	-----	667
Db	79418	GTGTCTCAAAACTGTATCGAGCGTTTCTCTGGCGCATGCAATGCGTGTCAACCCTCATC	79359	Db	78338	ATATGTTAGCACACTGGATATTGAAAAGCATCTGTACCACAGAGTACAACATAGATGTAC	78279
QY	627	-----	626	QY	668	-----	667
Db	79358	FTCTTATGAGGATTAAAGGATTCGTGTTATTGACCTTGTATCCGCAATCTTCAGCAACGA	79299	Db	78278	CTAATAAGGTCAACACAGACCCCTGAATTATGATGAAGTAGCAGACTAGCAATGGCAAAAG	78219
QY	627	-----	626	QY	668	-----	667
Db	79298	TGTTTTTAAGCCATAACACTCTATTGGTATCGTAAACGCACACATCTGCACAGGCTATGT	79239	Db	78218	CCAAGTGCACACCAGAAGTGTATAGTATTTGTGTACATTTGATGTGATTTCCCAAGATT	78159
QY	627	-----	667	QY	668	-----	667
Db	79238	GCACAAATGTAAGCCGTGAAGAGCTGTAGAGGAGTTTATTTCTCTCTCTGTTGTACCTG	79179	Db	78158	ATGCCATGTTTCAGTTATGTCTTTCTACACTTTTGTACCAAGCCTTATGTGAGTGTCTAAAC	78099
QY	668	-----	667	QY	668	-----	667
Db	79178	GGGTTGACGTTATGCTCGTATGACGATGCTTTATTCATCCGATTGGAGAGAGC	79119	Db	78098	ATCTTTGAATTTATCTGTGATGAGGATTTGCTCAGTGGCAGGTATTTAGTTTATGAGGATG	78039
QY	668	-----	667	QY	668	-----	667
Db	79118	TGTGCAATGAGCATCTACGGGTACAGAACATCCATCCATGCTGCTCTGAAAGAAATGTGATTG	79059	Db	78038	GTGAAAGACCACCAAGGAAAGGACTCAGTACACAAATTTCTGTCCCAACAAATAATAGAGTTGAC	77979
				QY	668	-----	667

Db	77978	TGAGATGGCAGTGTGTTTTTCCAGCTGAAGTTGCTACCTGGCTGGTGTGGTGCACG	77919	Db	76898	GGGANAAGAGGGAGAGAAAAGCACCCTTAGGGTCTATGAGTTTACTAGACGACGAGN	76839
Qy	668	-----	667	Qy	694	-----	693
Db	77918	TCGTAAAGCCTAGCAGCTTTGGGAGGCTGAGCAGGTGGATCACTTGAGGTGAGAAGTTGG	77859	Db	76838	TAGCCCCCTTATCTCTCTCTCATCACTCTGTGAGANTTATAANACAATGTGGTTGCTNT	76779
Qy	668	-----	667	Qy	694	-----	693
Db	77858	AGACCAGCCTGGCCACATAGTAGAAACCCCATCTCAACTAAATATACAAAATTAGCTGG	77799	Db	76778	GATAAAACNACCAGTAATCAATATATGCTGCTNTAAATACCTTAATAAAAAAATATTAAAA	76719
Qy	668	-----	667	Qy	694	-----	693
Db	77798	GTGTGTGACACGACACCTGTAGTTTCTACTCTACTGGGAGGCTGAGGAAGAGAATCTCTT	77739	Db	76718	GTCAGTNCCTATCTCCCTAATAACACAAAGAATCATTTTCATTAGTAATAATTTTGACG	76659
Qy	668	-----	667	Qy	694	-----	693
Db	77738	GAACCTGGGAGGTAGAGTTGCAGTGAGCTGAGATCACACCACTGCAAGCCTGGCCACAT	77679	Db	76658	TACACTTAATGATNGACTACTATGATTTTAAAAATATAAGATACCATAATTAAGCAAT	76599
Qy	668	-----	667	Qy	694	-----	693
Db	77678	AGTGAACCCCGTCTCAATGAATACACAAAAAATTAGCTGGGTGTGGTGACACGCACCTG	77619	Db	76598	GGGAAGGATGTGCTAATGATATGACCTTGTAAAGACACCACTCCAGCCTAGTTCTTCATTG	76539
Qy	668	-----	667	Qy	694	-----	693
Db	77618	TAGTTTCAGCTACTCGGGAGGCTGAGGAAGGAGAAATCTCTTGAGCCTGGGAGGTGGAGGT	77559	Db	76538	ATCAGCCCTGGGTTAGTGTCTCCAGCTTCAAAATGCACAGCCGTATCTATGCTTAAAA	76479
Qy	668	-----	667	Qy	694	-----	693
Db	77558	TGCAGTGAGTGATGATACACACCACTGCACCTCTTAACCTGGGTGGCAGAGCGAGACTCTGT	77499	Db	76478	AATTCGATGGCTTCTCACTCAAGACTAGTTTACATCAGAATCTCTGGGATAGGACACAGAA	76419
Qy	694	-----	693	Qy	694	-----	693
Db	77498	CTCAAAATGAAAATGGAGTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAA	77439	Db	76418	ATCAGTATACAAAC	76359
Qy	694	-----	693	Qy	694	-----	693
Db	77438	TAAATAATAAATAAAGTTGCTATCAACCTTATTTTAAACCTTAACATCTACAATCAA	77379	Db	76358	ACACACACACACACACAGGTGTATATATATATATATATATATATATATATATATATAT	76299
Qy	694	-----	693	Qy	694	-----	693
Db	77378	GACCTGGGCAGTATTATCCATAGATCTGGCAGTAGTGGAACTCTGCATGTTTACAGA	77319	Db	76298	ACTGAGAACCACCGATCTGGATTTTGAGGATATTTGAGGTTACAGCTCTGTTTAAATGG	76239
Qy	694	-----	693	Qy	694	-----	693
Db	77318	CTTTATCATAAATGCTCCTACCTCTGGCCCTGAACCTAGCCAGCAACCTCAAAGTGCCAGAG	77259	Db	76238	AAAGTTTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	76179
Qy	694	-----	693	Qy	694	-----	693
Db	77258	GGTTCCTGCCAATACGTTTCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	77199	Db	76178	CGTTTAAAGAGTTGTCATTCGAAAGAGACTCCCTCACCGGAAGCAGAAAGAAAGTG	76119
Qy	694	-----	693	Qy	694	-----	693
Db	77198	ACTTCTTAGAGACACAACATTTTAACTTAGCCAGGATTTACTATAATTTGAAAATAG	77139	Db	76118	TTAAAAAGTTTGGTTCTTTTTTCTCTGTAAGCCAGACATATCTAAAGACAGATTTGAACA	76059
Qy	694	-----	693	Qy	694	-----	693
Db	77138	TAAATATGAGCTAAATTTGTCATTAACAAAGACGATTTTATTTTATCAGTCCCATGCTT	77079	Db	76058	CTGGCAGATGTCAAAGAAAAGACTCAGAGATAGATTACATTAGAAAAGGGTTTACTTGCA	75999
Qy	694	-----	693	Qy	694	-----	693
Db	77078	TGGAGAGGAGATTCCTGAAGAACTAAAAGCAGGCTCGGAGCAAAAAGCCATGATGAA	77019	Db	75998	AAAGATGCGAGGAGTTAGACGGAAGGACTAGTTTGCCACCAGTACTTAAAGGGAAAAAA	75939
Qy	694	-----	693	Qy	694	-----	693
Db	77018	CTACTGNN	76959	Db	75938	AAATCCCTAAAAATTACCAGGATTACCGGTTGACAGTAGTCTGTTTCATGTTGAAAAACA	75879
Qy	694	-----	693	Qy	694	-----	693
Db	76958	TTTTCCACTTTGGCTTCCTATATTCCTTAAGCTACCTTCTGATATTGGATGGGTGAGA	76899	Db	75878	GTTAACTTCTCAGATGGGTTTATTTACTCACAAAGGTCAGGCCAATTTAATGTTTACA	75819
Qy	694	-----	693	Qy	694	-----	693
Db				Db	75818	AAGGTCAGAGGTTTAGCAAGGGTAAATTTTTTAGGGGGATTTTAAACATGTTTAAAGGG	75759

QY	694	-----	693	-----	693
Db	75758	AATTCAGGGAATATATTTCAAGGGTTTAATTTGGGTTTGGGAGGTTTCGGAATAAT	75699	-----	75699
QY	694	-----	693	-----	693
Db	75698	CCAGGGTGGATCCCTGGCAAGTTTTTTTGGGGGTAACTTCCCTTTTATAAGGCTTTG	75639	-----	75639
QY	694	-----	693	-----	693
Db	75638	GCCCATATTTGGAGAACAGGCCAAAGGCCCTCAAGATAATTTGGCTTTTAAAAATACC	75579	-----	75579
QY	694	-----	693	-----	693
Db	75578	CCTTTAAGCCACCAAGCTGGGTTCCAATCTCTGAAGGAAGTCCTCGGAATTNNNN	75519	-----	75519
QY	694	-----	693	-----	693
Db	75518	NNNNNNNNNNNTTATATTTTACTTAAACACACCCCTCAAATGTCCAAGCTTT	75459	-----	75459
QY	694	-----	693	-----	693
Db	75458	TCTGCCAATCTCCCGGCCGTACAAATTTTCTTAAGAAATTTTAAACTTCAACCTCT	75399	-----	75399
QY	694	-----	693	-----	693
Db	75398	GCCATATAAATTTCCACCGGAAGCAGCTGAGATTCCAAAGGGGGTTTGGAGCTTC	75339	-----	75339
QY	694	-----	693	-----	693
Db	75338	ATTTGAACAAGTATTTTACTTGAACCCCTGGGCTGCATCTGCCTCTAAGTTTTTTCT	75279	-----	75279
QY	694	-----	693	-----	693
Db	75278	TTCCCTCTGGCTTGGAAATGCAAAAGCTGGGGGCGCTGGTTTCAAGACGCTTCT	75219	-----	75219
QY	694	-----	693	-----	693
Db	75218	CCCTCTTTATGTGATACTTACTGTGTGTACCTGTGAACCACTGGTGAGGCGCG	75159	-----	75159
QY	694	-----	693	-----	693
Db	75158	GGAGATCAGAGCCCCAAGGCGCTCCCTGCTGCAGCCCCAGGATACCTGGGCTCACTC	75099	-----	75099
QY	694	-----	693	-----	693
Db	75098	ACCTCCCTTCTCTTGTCTGCAGGTTGGAGATGGCTGTGGGAATGCATCTCCTCAGAT	75039	-----	75039
QY	694	-----	693	-----	693
Db	75038	GAAGGTGTGCTGCGCCCCAGTTTCTTTCTGCTCTCCTGCTGGACTGCAGGCCCTCC	74979	-----	74979
QY	694	-----	693	-----	693
Db	74978	TTGCCCCCTGACCTTGAGGGGCTCTGTGGGCGTGGGAAGCTCTCCTCCACAGACAC	74919	-----	74919
QY	694	-----	693	-----	693
Db	74918	CCTTGGGTCTGTAGTAGTGTTCACGGGGCCCTTGCTGCATGTGTGGTGGCCAGGC	74859	-----	74859
QY	694	-----	693	-----	693
Db	74858	CGTGCCAGGCGCAGAGCCCTAAGGTGGCCTCCCTCCTCGCCCACTCCCTGACTCAAT	74799	-----	74799
QY	694	-----	693	-----	693
Db	74798	GGGCTTTTATTCCTTTTGGGAGGTAATTCATGCCACAGGTAGAGCCTGGGAGATGAGG	74739	-----	74739
QY	694	-----	693	-----	693
Db	74738	AATGTGGTGGATTTGGCCCTGAGGCCACGGGCTCCTGTGGCCAGTGTGTGGGA	74679	-----	74679
QY	694	-----	693	-----	693
Db	74678	GCTCAGAGAAGCGAGGCCCTTCCCTGGAAAGTCAGAGGGGCCCCAGGCCATTTCTCAG	74619	-----	74619
QY	694	-----	693	-----	693
Db	74618	CTGGGCTTTAAAGGAAGCAAGAGGGGATGAGAAGTGTGACTGCAGCCAGGATTTGGT	74559	-----	74559
QY	694	-----	693	-----	693
Db	74558	TGAGGAATGCTGGGAGAAAGAACTGGAAAGGTAGATTAGTTGGTGGGGGCGCTGC	74499	-----	74499
QY	694	-----	693	-----	693
Db	74498	ACTGGGAATAAATCCAGGGCTTACCATCCAGCAGCTCCCCCATGGTCCACCCCTACT	74439	-----	74439
QY	694	-----	693	-----	693
Db	74438	GTGTGTCCAGCCCTGCCTGTGTGGAGACTTACTTGGCTTCTTCTCTCCGAGCGGAA	74379	-----	74379
QY	694	-----	693	-----	693
Db	74378	GCCCGTTCTCCCTCAGGGCTTTGCACTTATCCCTTAGCCTGGAAGGCTTCTTCTCTGG	74319	-----	74319
QY	694	-----	693	-----	693
Db	74318	CTGTGCTGCGAGGATCCTTCTCTGTCTCATCTCAGCCAAATGCTGGTTCCAGACAGG	74259	-----	74259
QY	694	-----	693	-----	693
Db	74258	CCCCCTCCGCTCCTCATCCGAGCACCTCCCCCTTCTCCACACAGCTCTGCCTTG	74199	-----	74199
QY	694	-----	693	-----	693
Db	74198	TGTCCTCTGTGATTTTCTTCAAAGCACTCTCGCCATGTGGAGTTGTTTCTTTGCCCTACT	74139	-----	74139
QY	694	-----	693	-----	693
Db	74138	TGCTTTCTGCTTTTGGTATCTCTCCCATCCACCTGGAGAGTTGACTTCCCTCCTGGGG	74079	-----	74079
QY	694	-----	693	-----	693
Db	74078	CCCCCACTCCGCTTCTCCTGTGCTCAGATGCTGCCCTGGCTTGGTACNNNNNNNNNN	74019	-----	74019
QY	694	-----	693	-----	693
Db	74018	NNNNNNCACTTTACAAGTTAGGAAGCCTTACACATTATGGTCCAGGGATGCCATTCAA	73959	-----	73959
QY	694	-----	693	-----	693
Db	73958	GCAGACCACATGATAAAGGTGCTCCTTTGAAGTAAGCCCTGAATGTGGGGGCCCTGAAT	73899	-----	73899
QY	694	-----	693	-----	693
Db	73898	TTTATGCCAAATTTGCCCACTTATTTCCCAAATAATTTCCCAATTTCTGGTCATTTCTCT	73839	-----	73839
QY	694	-----	693	-----	693
Db	73838	CCATCTCAACGGCTAGTACTCTTGTTCAGGATACCATAATCTCTTCCCTTAGGTACCCCA	73779	-----	73779
QY	694	-----	693	-----	693
Db	73778	AGTCTCTCACAAAGTTCCCTCTCTAATGTCCCCAGGCAACTGTTCTTCCCATAGTAG	73719	-----	73719
QY	694	-----	693	-----	693
Db	73718	CCAAAGTAAATTTTATAAAATACAAATTTTCCAGAAATCACCCCTCTATATAAACTATCACTA	73659	-----	73659
QY	694	-----	693	-----	693
Db	73658	GTTCACAGTACCCCTCAGGATGAAGTTCAAATGTCTCTAGAAATCTCAACCTTCTGTCT	73599	-----	73599
QY	694	-----	693	-----	693

Db	73598	TCACGAGCTCATTTCTTACACAAATCCAGTTCOCACCTCTGCTGTAATAAAATTAACATTAA	73539	Db	72518	TTCTATCTTCCGCTGTGTCAAGACAAATGGTGTTCATTAAACCACCTTTCCCATCTACG	72459
Qy	694	-----	693	Qy	694	-----	693
Db	73538	GTTTTCTCAAACTGTCTGTGCTTTTGGCATGCTATTTCCTGGTATTTCCTCATGATCCCT	73479	Db	72458	TTTCAAACTAGAATGTTTTNN	72399
Qy	694	-----	693	Qy	694	-----	693
Db	73478	TAGTATTACCTGTTTAGCAATTTATTACGCTGTACCTCTTTATTATGTATCCCAACCATCCC	73419	Db	72398	TTCCAAGAAGAGCGCTTGAAAGTGGTTTCCAATAAAATGGATCTCCTCTCTTGGGGTGG	72339
Qy	694	-----	693	Qy	694	-----	693
Db	73418	ATCCACCTCCCTCTGCTTGAAGTTTGTGAGGAAAGATCCATGTTTACTTTGTGTC	73359	Db	72338	AGACAAGAGCCCTTGGCACAAGTTTCGGGGACACAGAGGGGAGAGGACGCTGGG	72279
Qy	694	-----	693	Qy	694	-----	693
Db	73358	TTTTTGTATTTTACAGTGCCTAGCAGTGCCTGGCATTTATATGTAGATTCAACAATATTTG	73299	Db	72278	TTTCCAAAATTTGCCAAGTATTACAACCTCAGTCGGCTTTGGGCAAAAGTACTTAACCCCT	72219
Qy	694	-----	693	Qy	694	-----	693
Db	73298	TTAAATTAATTAATGAATGAATCAACAAGTTTTCATTAAACATTAAATTTTAAATGTTT	73239	Db	72218	TCTGAGCGCCAAATTTTTCATACCTTAAATAATCGAAAGTTTACAATAAATCTCTTGT	72159
Qy	694	-----	693	Qy	694	-----	693
Db	73238	TTTAAACATAACTCTGATAAGGTCAAAACATTAAGAAAGCATTTGTAAGGTAATAATGA	73179	Db	72158	GAAAAGCGCCATTTGGAGATAATTTAGAACCTCAGAGAATAATCGCTGTGCCTAGTAG	72099
Qy	694	-----	693	Qy	694	-----	693
Db	73178	GCCTTGGTACTGTCTCAGAAATGCCCTCCTGTTAACAGAGATAATGGATTAGAGGTGG	73119	Db	72098	GACAAATGGTAACGTTGGAGGAAAGAGGAGTGCACAAACCCAAAAGTCAAGGACGTGA	72039
Qy	694	-----	693	Qy	694	-----	698
Db	73118	AAGTAAATTTTTTCAAAATGCGTTAACAAATTTGTTAAATGGTGAGGACTTGGATATGC	73059	Db	72038	AGGATTTTCCATAATTAGACTTGGCTTTGGCCCTAATTTTGCAGAAATGCAGAAAGCCAC	71979
Qy	694	-----	693	Qy	699	ACACACAGGAGGGGATGATTTGCCCGCCCTTACACATGTTGTCTTCTCCTCGAT	758
Db	73058	CCCATCAATTTATTAATGAGTGTACTAAACACAGAGTCGGAGGACCAATAAATGAC	72999	Db	71978	ACACACGAGGGGCAATTGGATTTCCCGCCCTTAAGACATGTTGTCTCTCTCTTGAAC	71919
Qy	694	-----	693	Qy	759	CCTTGGTCCAGGTGCCCTTACCTGAGCTCAGGTCAATGTGGCAAGCAGAGCCCTCTCGTG	818
Db	72998	GGCATGGTCTTCGCCAACAAATCAAGAATAATATGATGTAATTTGTTGCTATCAAGT	72939	Db	71918	CTTTGATCAGAGTGTCTTACTGNAAGCTCAGGTGAATGTGGCAAGCAGAGCCCTCTCGTG	71859
Qy	694	-----	693	Qy	819	GTGTGAATGTGTGTGGCGCCGTCTCTGGTGACACAGGGACCTCACAAATCCCTCCCT	878
Db	72938	CAAAAGATACAAATTAACAGTAAATAACTACATTTCCAGAAAGAACCACTTGGGAAATA	72879	Db	71858	GTGTGAATGTGTGTGGCGCCGTGCTCATGTTGACACAGGACATCACAATCCCTCCCT	71799
Qy	694	-----	693	Qy	879	CCAGGTCTCTCTCATGTCTCCAGCCCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	938
Db	72878	CTGCTTTTATACCTTTAAGGCAATAATATTACTATTATTATAAATAATGACTGAGCACTA	72819	Db	71798	CCAGGTCTCTCTCATGTCTCCAGCCCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	71739
Qy	694	-----	693	Qy	939	GGAATTTGCTGTGTTGGCTCCCAACACGAGCAGCCCTTCTCTGGCAGCAGCTGTGCCA	998
Db	72818	TGTACAGGCATTAATGTGCTAATACHTATTAAGTATTAGCCTTTCATAAAATCTTTGAGG	72759	Db	71738	GGAATTTGCTGTGTTGGCTCCCAACACGAGCAGCCCTTCTCTGGCAGCAGCTGTGCCA	71679
Qy	694	-----	693	Qy	999	TCAAAGTTGGGATAAAGTCCCTATGACATCTGCCGGCCAGCACCACTCAGTGTGACC	1058
Db	72758	TAGGCATTTACTAATAATCTATTTTATATGCGCGAGACGGAAGCTTAGAGGTGCTAAGC	72699	Db	71678	TCCAAGTTGGGATAAAG-----	71661
Qy	694	-----	693	Qy	1059	TGCAGTGCCTGTGACAGCCCTCCGTGAGAGAGTGTGGCAGCGTTGGCCCGAGGATG	1118
Db	72698	AGTATGCCAAATTCACAAGCTAGTTGAGTGCAATAGGGTGTATACGACAGGTTAATTGAC	72639	Db	71660	-----GTTGGTGTGTGTGCGCGTGGGCACAGCCGACA	71626
Qy	694	-----	693	Qy	1119	GCTGGCCAAAGGGCAGGTG-----	1138
Db	72638	CCAATAGCTTTTATATACCATGCTAATTTGGGATAAGGAACCATATGTCAGCCCTA	72579	Db	71625	TCGACCCCTGCTCTCTCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	71566
Qy	694	-----	693	Qy	1139	-----	1138
Db	72578	AGGCTGCTTATTAATCAATCACTTTTATTAATGATTTGGTATGTTGTTATATATAGTACCGGAGC	72519	Db	71565	CCTGGCCAAAGTGGCAGCCTGACTCCTCAGGCTGTGTGTTCCAGGCTGCTGCTGCTGCTG	71506
Qy	694	-----	693	Qy	1139	-----	1138
				Db	71505	CTGCTCCTACCTGCCTCTTTTTTGTGTCAGGGGCTCCCACTGCAGCTTTCAGCTCTTTG	71446

QY	1139	-----	1138	QY	1295	-----	1294
Db	71445	GGGATCCCTTCCAACATTACTGCAAAATAGCCGCCCTTCTCTCCCTGGGGTGGAGA	71386	Db	70365	TGACTCCCCAGCTACCCCTGTGTGTACTGAAGACAGAGAAGTTATGTCTCTTTTCTGTATGC	70306
QY	1139	-----	1138	QY	1295	-----	1329
Db	71385	TCAGGSCCAGCCCTTCCCAAAAGCTCCAGTTCTTGGTCTTCTTTTCCAGTCCCTTAAT	71326	Db	70305	TTAATCCCTACTGGGTACATTATAGACACTTTAAGAAGTGTTTGAATGAATGAATGCCCA	70246
QY	1139	-----	1182	QY	1330	GGG-----	1332
Db	71325	GAACCTTTTGTGCGGGCAAGTACAACTCAGTGTGTGAACCCCTGCCAGCTTCCCTGGTT	71266	Db	70245	GAAGTCTGTGGATTTTCCCACTACATATATTTTAAATCCATCTTGACGGCTGGGA	70186
QY	1183	-----	1182	QY	1333	-----	1332
Db	71265	GAANAAGCCTTCGGGTGTAGAAAAGTTGTATTGGCTTACCCTTTGGCCCCGAGGTAGGG	71206	Db	70185	TGCCATATAATCCAGCACCTTTGGGAGGCCAAGACGGGTGGATCACTTGAGGTGAGGACT	70126
QY	1183	-----	1182	QY	1333	-----	1332
Db	71205	TTTGGCCTTGGCCCATPAGGCGATAGTTCTCTGGTGAAGGGCTCATTTTCTCACGTG	71146	Db	70125	TCGAGACCAGCTTGCCCAACATTTGTGAAACCCCGTTTCTACTAAAAATATAAAATCAAG	70066
QY	1183	-----	1197	QY	1333	-----	1359
Db	71145	TGTGAGATTGTGTCCTCCCTGAGATTATCCCTCCAAGTGGACGGGTGGCGCCCTTGGGT	71086	Db	70065	TGGGTGTGTGGCGCATCCCTGTATATCCAGCTACTTGGAAAGCAGAGGCTGGAGANTCG	70006
QY	1198	GGCCACATCTGGGGCTC-----	1216	QY	1360	CTGGAGCC-----	1367
Db	71085	TTCATGTCTCAGGGTCTCCCATTTTCATGACTTATTGCTCTACTCTTTTCACAATCTTT	71026	Db	70005	CTTGAACCCCAACAGGCTGAGGCTGCAGTGACGAAGATCGACCATTTGTACTCCAGCTGG	69946
QY	1217	-----	1216	QY	1368	-----	1367
Db	71025	TCTGTGCTTCCCTCCGTTGTGATTTGTATGGTCTTCCCTTTTATTGGTGAAGTGG	70966	Db	69945	GTGACAGGAAGACTCTGTCTCAAAAACAAGAAATAAAATCCATCCTGCTTCTTTTATAC	69886
QY	1217	-----	1216	QY	1368	-----	1367
Db	70965	AATTCGGTCTGTTTCGAAGCTTGACTTCTCATTTGCTGTGTGTAATGAACATATCCTCT	70906	Db	69885	ATCCAAAAGAAATAACATAGATGGTGGTGGGATGTGGCTTCTGAAATCAGACTACTTGTG	69826
QY	1217	-----	1216	QY	1368	-----	1367
Db	70905	GTAATCTGTGTGTGTCTATTTCGGGCACACCCCTTTTACGCTTCCACTTTTGTGTG	70846	Db	69825	GTACAGTAGTCTTACTGTCTCCACCACCTGTTAATCAGATGTCTATGGCAAACTATATAA	69766
QY	1217	-----	1216	QY	1368	-----	1377
Db	70845	TCCTTGTGCGGTTTNNNNNNNNNNNNNNNNNNNGAACATAGTTCATCAATCAGCCAT	70786	Db	69765	CCTATATATGCGTCAAGTTCTTCTTAATCTCTAAAAATGAAATCCTTGAGTGTATCTTGATC	69706
QY	1217	-----	1216	QY	1378	TATCCACAGTGG-----	1425
Db	70785	AGAGAAGGCCAATGTTAGCACCTAATGACATCTAAGATGATGTCACGACCCCTCCAGGAGCT	70726	Db	69705	TTTCAGAAAATTGGCCCTTTTGTACAGCAAAAGGCCCTTTCATTAATCTGGCTCCTACTTCT	69646
QY	1217	-----	1216	QY	1426	GGGGATGTACACACCGCCAA-----	1446
Db	70725	TAAATCTAGTTATGTGCACACATGAAAATTAACAAATAAAAAAGGGAATGTA	70666	Db	69645	TCACCATCTCCCCACAGCCCAAGCCCAAGTACCTCCAGTGCCTGCAAAATCCCTAAATGTT	69586
QY	1217	-----	1216	QY	1447	-----	1446
Db	70665	CCAGTCAACTCAAACTCTATCCCCATGTCACTTCCACAGTATACAGAAGTGCCTACAC	70606	Db	69585	TCCTGTTTTTCATACTCCTCTGTTCCAAGCTGTCTACCTAAACCATGCTTTCCCTGCATC	69526
QY	1217	-----	1260	QY	1447	-----	1446
Db	70605	CCCAAGGTCAAGTCAAGGTGCTCATGACTATGCTATTAATACATGGCCTTCACCTATGCT	70546	Db	69525	TGCTGGATTATTCCTTCTAAATCCTTCATGCGCTGAGACTAGATGGCTCCTCTGCACAGAT	69466
QY	1261	GATCCACACAGCTGACCGCTGGGCGCCACTGTG-----	1294	QY	1447	-----	1446
Db	70545	GATCCTGCCACCTGGACATCTCTTCCCTGTGACCTTGGACCATCTCTCAAGTCTC	70486	Db	69465	GCCTTCTCAATCCTACCAGTTGAGCTTTGAGTCTGCGCTCTTAGACTTCTATCATTTATA	69406
QY	1295	-----	1294	QY	1447	-----	1446
Db	70485	ATAGAAATGCTGCTCTTCCCTTCCCTGTGCCACCCAGTCTGATTGAGAGCTGCCCTTGG	70426	Db	69405	TTTGGCACCTTTTATTATAGTTTCAATCTTTTCTTCCAAATCCCTTAATAGACTGAGATAC	69346
QY	1295	-----	1294	QY	1447	-----	1446
Db	70425	TGCTCTTTCCAAACCTTTATTAGGCACTCATGACACTGTGCTGTAATTGACAGATTTATT	70366	Db	69345	TTTACGGGTAGAGGCTGTGGCTTAGCATAGCAGCTGGCACATATAATATGTGCTGCTGAATTA	69286

Db	69285	AGAATTAAATCCACAAATCAGAAAGCCCTTGGTCAACAAAGTTGTCCTCCAACTTTAACTC	69226	Db	68205	GTGGATGGTGTCTCAATGATCAGAATAGCGACAGAGATGGTCAGTTGTCTCTCTGTGG	68146
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	69225	AGAAGATGGCATCACAAGAATCTTGTGATGACTACTNNNNNNNNNNNNNNNNAAAGG	69166	Db	68145	AGGTCTGGAGAGTTTGGAAATATGCTGAGGTCTTTGGCAAGGATTTGGGAGGCACTCAG	68086
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	69165	ACACAGACACAGGGTTAAACGGACCCTCAAGAGAAATACACCCTTAAGACCCACGACATT	69106	Db	68085	CTGTGACAGACATAGAGGTGGGAATTCATCAGCCAAATATTTATCGAGTGCTCCTACATACA	68026
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	69105	GATGCCAATCCACGTGTGTAACAAAGGTTACCATAGATTCACACTTAACTTAAATAGG	69046	Db	68025	CATCAGGGGTATGCTCTTATTGGACTGGCAGGGTTTCAGGCTAGGCTGGAAAACTCTTCC	67966
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	69045	ACAATGGCCACATTTATACAGATAAAGAACTGAGCACAGAAAGGTTAGGAGAGCTGCC	68986	Db	67965	TGGAACGATTGGTTTCTGTGGGACAGAACCCAGATAAGCCTCAGCATTAGGSCATTGT	67906
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	68985	AAAGCACAAATCATTAAATTATGCAGCTGTCCCTAACCCAGATCCATCTGACAGGGGTC	68926	Db	67905	TTGNAGTAGGCCTCATTTCATCTCTGGGCTACCACAGGTGTCTGGGTCTGTCTCAGGATCAA	67846
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	68925	ATTCTATAGCCACCGTTGCTCCATTGCCCCACAACATCACACTTTGAACGACAACCTAA	68866	Db	67845	CAGCCCTTGAGAGAGACTGACCACAGAGACTACTAAAAAGGACACCTGCCCCAGGCCAGCC	67786
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	68865	TCATGCTCTGTTACTATACAAAGCAGTCTAGATTAAATTCACCTGGAATTAAGGGACCT	68806	Db	67785	TATCTTACCATCTCTGTTCTCTGCTGCAAAACCAAGGCCACGTCAATTCAGCAGAGGACCTG	67726
Qy	1447	-----	1446	Qy	1447	-----	1446
Db	68805	CAAACTGCCATCTAGTTCCACTTCTCATAGATGTCACAACTCCCTTAAACAACCCCTAAGT	68746	Db	67725	CGTGTGAAGGACCCCTGCAGCTGCCCATCACAGGAGAGCCCAAGACTCACCTCCCAAGG	67666
Qy	1447	-----	1446	Qy	1447	-----	1480
Db	68745	GCTTGCTCCTCCTCCTCCTCCTGCTGCTGAGGGTTGAGGGGTGGGAATTGGG	68686	Db	67665	GGACCCCTGGCACATGAAGATGCTGGTTCTCTGGGACTGTGCTGCCCTGGCCACAGGATAG	67606
Qy	1447	-----	1446	Qy	1481	CAGTACTGGTGGCCACCGAGCTGT	1505
Db	68685	ATATGCCCTCCCAGGGTGCTCATACGCCCTCTTTCGCAGATCGGATTTCCAAACCCACAGA	68626	Db	67605	AAGCGCAGGATGGTCAACCATGCTGCTCTATTGAATGTCTTTAGAAGCGGCTCCATG	67546
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68625	TTTTATAACGAAGACATGCTGACAAGGCAGAAATAATCCATTAGCCCAATAAATGAAA	68566	Db	67545	TGTGATTCTTTCCAGCATTGGTTAGTATGGTGTATACCATGATGAACTACTGTNNNN	67486
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68565	ATATATCAATACATATTTCATGCAAAAGATGCTCATAACTTAGATGTCCATGTATGTGTG	68506	Db	67485	NNNNNNNNNNNNNNAAGAAAAATAAAGATTCTTATAGCACAGTTGCTTCTCGGCCAA	67426
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68505	TATACACACACACACACACACACACACACACACACAAAAAGAGAGAGAGAGAGAGA	68446	Db	67425	GAACCTGCCCTTATGAGTGTAAAGTAAATAGCAGCTTTAAGAAAAATACCAATAAGGCTAAT	67366
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68445	GAGAGAGAGATACATTAGATAGATTTCAGGCAGCTTTCTCTCCCTGCTAGCCTGTT	68386	Db	67365	CTTACCAGAGTGGTTGTTCAAACCTCTGCAGACCATTAAGACTTCAGCCCAATAAGCAATC	67306
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68385	GTGGACCAAGAACTCTGCGCTCCTCTTCTGAGTACCCCGCCATTAGGTACTCACAT	68326	Db	67305	GAATTACAACACTACAAGTGAACAAATGCCAGAGAAATTACAAGACTTTATGCGGATNTAG	67246
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68325	GGGCTTTCCATCTTCAGACTTCCCAAGAACCCACAGTGGGACCAGCCAGCAAGTTGGG	68266	Db	67245	AAAACTGGGAAAAAGACATTANACAAAAGGATATGGAACCTAAGAGACAGAGATGGTGCC	67186
Qy	1447	-----	1446	Qy	1506	-----	1505
Db	68265	AATTGTGTAGGCTGGGTCTGTGAGAGCTGGGTAGGAGAGAGTGGAGGAGATGCATG	68206	Db	67185	TGAAGAGTAAATTAGAATTCGTAATTAGATCCACCACCAAACTAATTTTATAAAAATAA	67126
Qy	1447	-----	1446	Qy	1506	-----	1505
Db				Db	67125	AGCATAACTTTTAAAAATGTTTTGTGAAAAATACTGAAATGAAAGTGACTGCTTCACTGT	67066

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QY	1594	-----	1593	QY	1594	-----	1593
Db	62685	CTAGGTATTGATGGAATGTTCTCAAATAATAAGAGCTATTATTATGACAAACCCACAGCC	62626	Db	61605	TGGCAACAAATTTGTGTTTCCCAAATTTAAGCCAAGCCCCCTTTGTCCCCAACCTTTTTA	61546
QY	1594	-----	1593	QY	1594	-----	1593
Db	62625	AATATCATACTGAATGGGCAAAACTGGAAGCATTCCTTTTGAAAACACGACACAGACAA	62566	Db	61545	GGCAAAAGGGGAGAGAGAAATTTGTGTTTAANGAAATGCAAAATCCNTGCTCCCTTCAA	61486
QY	1594	-----	1593	QY	1594	-----	1593
Db	62565	GGATGCCCTCTCTACCACTCCTATTTCACACAAATGTCGGAAGTTCTGGCCAGGGCAATC	62506	Db	61485	TTACTTTTTCANTCAAAAAGTTGCCAAGAGGGCANAGANATATTGACACAGGGGAANGG	61426
QY	1594	-----	1593	QY	1594	-----	1593
Db	62505	AGGCAAGAGAAATAAAGGTATTTCATTTAGGAACGAGGAAGTCAAAATTTGTGTCT	62446	Db	61425	ACCAAAGATNNTGACAAATTTGAANGAGGGGACAGTGTGAAGAGGGAGCATGGCAGGTGTAT	61366
QY	1594	-----	1593	QY	1594	-----	1593
Db	62445	TTGCAGATGACATGATTGTATATTAGAAAACCCCATCGTCTCAGCCCCAAAATCTCCTTA	62386	Db	61365	AACGGTCTGTGCNTGGGTGGGTGTCGGAAGGGCNGCGCCTNTGAGAGCTCTCTCCAGCA	61306
QY	1594	-----	1593	QY	1594	-----	1593
Db	62385	AGCTGATAGGCAACTTCAGCAAAAGTCTCAGGATACAAAATCAATGTGCAAAATCACAAAG	62326	Db	61305	CCAGCACACATTTGGCATGTTCTTCCAGCCGCATGGTCTTTGCCCTCCACATCCTCGAGAA	61246
QY	1594	-----	1593	QY	1594	-----	1593
Db	62325	CATTCTATACACCATTAACAGACAAGCAGAGACAAATCATGAGTGAACCTCCCATTTA	62266	Db	61245	CAGGCCACATCCCATGCTCAACTCATGATGTTTCCAGCTTTAGACCCCTCTCATCTACCTCG	61186
QY	1594	-----	1593	QY	1594	-----	1593
Db	62265	CAATTGCTACAAGAGGATATACAAATTTGCTACAAAGAGAAATAACATACTAGGAATCC	62206	Db	61185	TTCAATTCAGCCCTGAGCCCATGAGGCCCCACAGGACCCACAGCCCTTCTCCACCT	61126
QY	1594	-----	1593	QY	1594	-----	1623
Db	62205	AATTCTCTCAAGGAGAACTACAACCCTGCTCAACGAATAAAGAGGACACAACAA	62146	Db	61125	CGGACTTTGGTCCACCTCTCTCAGCCTTCCCTACCTTCCATGATCTCGCTCCCCACAG	61066
QY	1594	-----	1593	QY	1624	CAACTGGCCATCAGCCGCTAGCCACACACTTGGGAGCGGTGCTCTCAAAAGTCCGGA	1683
Db	62145	ATGGAAGATATTCCATGCTCATGGATAGGAAGATCAATATTGTGAAAATGGCATACT	62086	Db	61065	CCTAGTCCCCCGCCCTGCATGCCATCTCTCCCTGGTCTCCACACTGAGCCTGAAG	61006
QY	1594	-----	1593	QY	1684	GCTGTACTC-----CGCCCTCGAGAGGCTGCTGGATCCCTCATGGAAACCACCGGTAT	1736
Db	62085	GCCCAAGTAATTTATAGAAATCAATGCCATCCCATCAAGCTACCAATAAATTTCTTCA	62026	Db	61005	TCACTGGTCTCACTGAATCTCTTGGCTTATGGTTTCACTTCTCACACACACCCAG	60946
QY	1594	-----	1593	QY	1737	ACGGACTGGCCCTCGCCAAAGCTCTCCCTCTGTCATCCCTTTCATGCTC-----	1785
Db	62025	CAGAAATGGAAAAAATCTATTAAAGTTTCATATGGAACCAAAAAAGAGCCACATTGCC	61966	Db	60945	GGCTATGGTCCCACTGCCAGCTCTATAGCCCAAGCATCTCTTACCTGGCCTCTCTTAC	60886
QY	1594	-----	1593	QY	1786	-----	1785
Db	61965	AAGACAATCCTAAGGAATAAGAACAAAGCTGGAGGCATCAGGCTACCTGACCTCAAACTA	61906	Db	60885	AGGCCCTCTGCTCTGGTCCCTACTCTCTCTCCACATCACTTCTCTGGACGAATGGCCCC	60826
QY	1594	-----	1593	QY	1786	-----	1785
Db	61905	TACTAGAAGACTACAATAACCGAAACAGCATGGTACTGGTACCACAAACAGAGATAGAC	61846	Db	60825	TGCCCCCACCACCCAGCAGCACCCTTGATGATACGGTTGAAGTCTGCTGTGTCAC	60766
QY	1594	-----	1593	QY	1786	-----	1785
Db	61845	CAATGGAACAGACAGAGCCCTCAGAAATAACACCACACATCTAAACCATCTGATCTTT	61786	Db	60765	ACGAGGAAATGACAGTTGTCTTCTCGCAGGATGATGGTGGCTGCCCGGGGTGCATCAT	60706
QY	1594	-----	1593	QY	1786	-----	1833
Db	61785	GACAAACCTGACAAAAACAAGAAATGGGAAAAGGATTCCTATTTAATAAATGGTCTGG	61726	Db	60705	CACCAGAGCCAGCTGTCCAAATCATCTCCCTCATGCAGGGTGGTCAACCAGCCCTGCG	60646
QY	1594	-----	1593	QY	1834	-----	1833
Db	61725	GAACCTAGCCATATGTAGAAAGCTGAAACTGGATCCCTTCTGATGATCGGTGNN	61666	Db	60645	CCAGGCTCAGTCTCAGCCCCGCCCTTGCGGCCCTGCCGCCACAGCTCTTTGCCAGGACA	60586
QY	1594	-----	1593	QY	1834	-----	1833
Db	61665	NNNNNNNNNNNNNNNNAAAAACACCTTTGGGGGAAAAATCTTTTAAAAATATCTGAAAT	61606	Db	60585	GACCCACGGCAGGAGAACACCCACAGGAGACACAGGGGTGAGCAGCAGTAGATCAACA	60526
				QY	1834	-----	1833

Db	60525	AAGCACTGCCATGAGGACATGGACCAGGAGAGATTAGACCCAGGGCACTGGGGTGG	60466	Db	59494	TTTGGTGGTTTCAAAATTGGGGACATTTTACCCCAATTTACAAATTTATAGGGGATAATT	59435
Qy	1834	AGTGGAGATCTCATCAACTTTGAGAAGATGAGAATGATGCCAGAGCCGCGGGATGCT	1893	Qy	2118	-----	2117
Db	60465	GGAGGAGGGGCTCACCTTGCCATGGGTACACAGCTTACAGATCCCTTCCAGATAAT	60406	Db	59434	AATTGGGAAGGGGAAATTTTAAACCCCTGCCAATTAATGATGNTCGTGGTAAATTTGGAC	59375
Qy	1894	GCACCA-----	1899	Qy	2118	-----	2117
Db	60405	GTACCAGAAAGTGCCCTTGTCGCCCTGGCTGAACACTGACAGAAGCATACCTCAGACCGG	60346	Db	59374	TGNTAAATGATGCAGTTCNTCNTAGCATCATGGGTCTTTACAAATTTGCCCTGTTTTGTC	59315
Qy	1900	-----CTGCGGAAGCCACAAACCTGTGCC	1923	Qy	2118	-----	2117
Db	60345	GCCTCTCGGACCTACCATTCCTTACACATCCTTCTGCCCATGTCCAGGCCCTGTGCC	60286	Db	59314	AGTGGCTGGTACTGGTTGTTTCTTCCATGTTTAGTGCTTCCCTTCAGAAGCTCTGTGAAG	59255
Qy	1924	TCCTCTACCACTCAGAAAGCGAGTTTCCACCTCCAC-	1960	Qy	2118	-----	2117
Db	60285	TGGCTTCTATGCTCTGACTTACACAGGTCCCTGCTGTGTGTTCARAAGA	60226	Db	59254	GCAAGCCGGGTGTGACACAATCTGTGTCAGCATTTGCTTGTCTGTAAAGGATTTTATTTCT	59195
Qy	1961	-----	1960	Qy	2118	-----	2117
Db	60225	GCAGAACAGCGCTAATCTCGCTTCACCTGTGTGTGGTAGAGATAGGAGAGTCGGTGGCGA	60166	Db	59194	CCTTCACTTAGGAAGCTTAGTTGGCTAGATATGAAATCTGGGTTGAAATCTTTTCA	59135
Qy	1961	-----	1960	Qy	2118	-----	2117
Db	60165	CAAGTTCAATGCGAGACGCCAGGCTTTTCTAGGGTGTGTAGTCCAAAGACACA	60106	Db	59134	TTAAGAATGTGAACATTTGCCCTACTGTCTTGTGCTTGTAGGGTTTCTGTGAGAGA	59075
Qy	1961	-----	1960	Qy	2118	-----	2117
Db	60105	ASTGCTGGGACAAAGATGTGCCAGGTGAGTGTTCACAGATTTCAGCAGGAGACAAA	60046	Db	59074	TCCTGCTTAGTCTGATGGGCTTTCCTCTGTGGATAACTCGACCTTTCTCTGCTGCTGCC	59015
Qy	1961	-----	1960	Qy	2118	-----	2117
Db	60045	GCAAGTGGAGAAATGGCTGAGAGAGCGGAAGATTTCAGACAGGGCAGCGCGGG	59986	Db	59014	CTTAACACATTTTCCCTTCATTTCAACCTTGTGTAATCTGACAAATTTGTCTGTGGGTT	58955
Qy	1961	-----	1960	Qy	2118	-----	2117
Db	59985	GCAAGAAATCAGACTGAAAATTTCCAGCCATAGATGGAAGTGGAGAAATGCCCTGTGCC	59926	Db	58954	GCCTTCTCGAGGAGTATCTTTGTGGCATTTCTCTGTATTTTGTGAATTTGAATGTGGCC	58895
Qy	1961	-----	1960	Qy	2118	-----	2117
Db	59925	CAGCAGTTGAGTTTCAGGAACTCACAGGAAGAGATGCTGTGACGGGCGAGGGCT	59866	Db	58894	TGCTTCTAGTGTGGGAAGTTCTCTGGATAATATCTGAAAGTGTGTTTCCAATGTG	58835
Qy	1961	-----GAGACAGCAGTGGCGAGGATTTCCATGCTCGAGCAGTCCCTGAG	2010	Qy	2118	-----	2117
Db	59865	GGGAGGGCAGAGCTGACCGAGTTGGAGAGGTGGGCCACACAGCCTTG	59820	Db	58834	GTTCCATTTCTCCCATCTTCAGGTACACCAATCAATGTAATTTGCTCTTTTCCACA	58775
Qy	2011	CACCCGAGTCCAGCCAGCACCTGGGCTTATGTCCAGCAGCTGAAGTCAATTCACACCA	2070	Qy	2118	-----	2117
Db	59819	-----ATGTGCAGCAGCTCCTCAAAGATTA	59795	Db	58774	TAGTCCCATATTTCTTGGAGGCTTGTGTTGTTTCTTTTACTCTTTTCTTAACCTGT	58715
Qy	2071	GCGGAACTCTCCGCTCTTCCGAGAGCTGGAGCCATGAGGAGG-	2117	Qy	2118	-----	2117
Db	59794	GCTCAGCTCTTCATCCGTGCGCTTGACTTGGCTGCAAGACAGGAGGATGGAGCACA	59735	Db	58714	CTTGTGCTTTTATTTCAATTAATTTGATCTTCAATCACTGATACCTTTCTTCCACTTAT	58655
Qy	2118	-----	2117	Qy	2118	-----CTGGAGCTGGAGCTGGAGCAGCTTCGAGCCGGGAAGCAGGCTGTGCCGGG	2172
Db	59734	CTGTAACTGTGGCCCGTTTCAAGTGTCCAGGGAAGCACTTCTTACCAACCAAGCGAATG	59675	Db	58654	CGAATCAGCTACTGAAGCTTGTGCATCATCAGCAAGTTCTCATGCCATGGTTTTCAAGTT	58595
Qy	2118	-----	2117	Qy	2173	CCA- 	2175
Db	59674	CCTGTTGCAAGAGNGTGCTTTTCAGCAAGTGGCAGTTTATCAACAAGCAACTAAGCCTT	59615	Db	58594	CCATCAGTCATTTAAGGCTCTCTCGACTGTTTATTTAGTTAGTCAATTCGCTCAATCT	58535
Qy	2118	-----	2117	Qy	2176	-----	2175
Db	59614	TTACCTGATGGCCACACATGTCCAATCGCTTTTGTATTAACAATNNNNNNNNNNNN	59555	Db	58534	TTTTTCAAGGTTTTAGTTTCCATTATGATGAGTTTGAACATCCTCTTTAGCTGGAGAA	58475
Qy	2118	-----	2117	Qy	2176	-----	2175
Db	59554	NNNNAAACGCACAACTGGATGGGGCCCTTAACTCTTATCCAAAAATTTGCAAGCC	59495	Db	58474	GTTTGTATTACGAGCCTTCTGAAGCCTACTTCTGTCAACTTGTCAAAAGTCATTCTCGTC	58415
Qy	2118	-----	2117	Qy	2176	-----	2175
Db	59494	-----	2117	Db	58414	CAGCTTAGTTCCATTCGTGGTGAGGAGCTGTGTTCTTTTGGAAAGAGAAATAGGTGCTCTGA	58355

QY	2176	-----	2175	QY	2176	-----	2175
Db	58354	TTTTAGAAATTTTCATCTTTTGTGCTGGTTTCTCCCATCTTTGTGGTTTAAATCTCCC	58295	Db	57274	CGCCCGACACATAAATCTATGCCCGCTCCGGAAATTTCTGGCTCCTGCCACCACACGGT	57215
QY	2176	-----	2175	QY	2176	-----	2175
Db	58294	TTTGCTCTTGATGTTGGTACCCTCAGTTGGAAATGTAGAAATCACCCCTTCTCTCGCGTT	58235	Db	57214	GGAAAGCTCGCTGATAGAGTCCACCCGCAATAGCATGGATGCCACTAATAAGCGCATGCT	57155
QY	2176	-----	2175	QY	2176	-----	2175
Db	58234	GATCAGCTGGAGCTGCAGATTTGGAGCTGTGCCTATTTCGGCATCTTTGGACGCCCTC	58175	Db	57154	GGAATCTGTCCAGCAGAGATGATGAGCGTTTCTGACGGTGTATGCGTCTGCCCTTATT	57095
QY	2176	-----	2175	QY	2176	-----	2175
Db	58174	AACTCGTAAGGAAATGTTGAAATGCTTACTGGGCACTTTTTTGTTTTTTTTTTTA	58115	Db	57094	CCTCCGATGATCCTGCCTGTTTCAGTTGGGGCAGCTACCCGCTGATCGGTACCTTCAT	57035
QY	2176	-----	2175	QY	2176	-----	2175
Db	58114	GAATCTTTAAAAAFACTTCCCTAGGTTTACTGATGATAGGGGAATTTAGCAGCGTTT	58055	Db	57034	TCCGTTACGGGTGACCAGTCCGACATCTATGAAGTCTTTAACGTGGCAGGTTTCTCTT	56975
QY	2176	-----	2175	QY	2176	-----	2175
Db	58054	AGAGTTTGGGTAACCTTTTAAATGAGTAATTTAAATTAACACTTTCATGTAAATATT	57995	Db	56974	TGGTCTTATGCTGCTGGTGATGTTCTGGACATGCAATCCGTCGGTGTGTACAGCCAGTT	56915
QY	2176	-----	2175	QY	2176	-----	2175
Db	57994	TCGCTATTCTCTTATATTAAGGGTTTCAAGCAGTTTACATTTTATAGAAATTTAA	57935	Db	56914	ACGTCCCGCTATGTGCTGGTGGCAAGCTCCGATGGCACCAGCAAAACCGCAACCTTCAA	56855
QY	2176	-----	2175	QY	2176	-----	2175
Db	57934	TGCTGTGATTTTATTACTGTCTTTTCTGAAGTTGGGATAAACACCCCTTGCATCAAG	57875	Db	56854	GATGAAGACTTCGAAGCCAGAATGTACCAATCCGAAAGTGCACACTAACATCTAGCT	56795
QY	2176	-----	2175	QY	2176	-----	2175
Db	57874	TAAATTATGAATATACATACAGAAAAAGTACGCAAGACAAATTAATTTAGAGAATAAT	57815	Db	56794	TAACCGTATTAACTCTGTTGTTGATAACGGTTCCGGCAGCCTTACTTCGTTTACTAA	56735
QY	2176	-----	2175	QY	2176	-----	2175
Db	57814	TACAAAGTGAACACCCATGAATCACCGAGTCAGAAATTAAGACATCACCCCTAAAAA	57755	Db	56734	TGCTCTGTGTAGCAAAATCACTGTTACCTGCTCTCTGAACATAACAATTTGGTCAGATTGC	56675
QY	2176	-----	2175	QY	2176	-----	2175
Db	57754	CCTCTCTATGTACCCCTGACTGATCAAGATCCTCTTCTCCCTCTTAAACTGTTATGCA	57695	Db	56674	CCTGTCTTCTCCAAAGCCGGATAAAGGCACACTGAGATTCGCAATTTGAGACGGAATCAA	56615
QY	2176	-----	2175	QY	2176	-----	2175
Db	57694	TAGACGATCCTTTGCATTAACAGTTTCTTCATTAGAAAATAACAATTTCATAGGAAGTCA	57635	Db	56614	TATTGAAGCCGCTCCTGAGCTGATCCCGTGTATCAACCACGAAATGAAGAAATACACCT	56555
QY	2176	-----	2175	QY	2176	-----	2175
Db	57634	GAGGAGTATTTTATCCTCTTTTATAAGGCAGAAAAGAAAGTTGTTTGTCTATGT	57575	Db	56554	GTTCCTCAAGTCAGTTTCGTTATCGCGCTGAGCACAGGTACAGCGCGGTATGAAGCACA	56495
QY	2176	-----	2175	QY	2176	-----	2175
Db	57574	TTGACTAGTAGTAGCAAAATAGATTCTTACTTTAATACTTTTCCAGTGCAATTTAA	57515	Db	56494	CGTGAAATTTGCTCTGGACCTGGTTCCCTACAGTTCCGCACCCTCAAGGAATACCTGTC	56435
QY	2176	-----	2175	QY	2176	-----	2175
Db	57514	TATGACTGATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAACTACTNNNNNNNN	57455	Db	56434	TCATGAACAGGATATGCTGCGTTTCGCATCATGATCTGGCGCACTCTTGGCAGCCGACAC	56375
QY	2176	-----	2175	QY	2176	-----	2175
Db	57454	NNNNNNNNACAGTAGTTTCATCATGGCAGTTCGGTACTGATGAACCAATTCATTAAAGA	57395	Db	56374	TTTGATCGCTCTCCCGTTTAAACAGTCCCTTTGATGATATGGGCAACCATCATTCGTGGC	56315
QY	2176	-----	2175	QY	2176	-----	2175
Db	57394	TGATCCCGCGCTGCCGATCTATCCTTGAAGCTGCACGTAAAGCCGGTTTTTGGGG	57335	Db	56314	AAATCCAGACTGTATATCGCGCATTTATTGAGCGGTAAATCTTCTGTCGCGATGGGG	56255
QY	2176	-----	2175	QY	2176	-----	2175
Db	57334	TATCTGTATAATGCCACCGCTCAAAATGGCTACAGCGTGGCAAGTGCACCTGGCTGACTA	57275	Db	56254	ATGTTTGTGCTGCTGATGTCAGCATCTTTCTTCAAACAGTTCCGGAAGGATTTCTCCAG	56195
				QY	2176	-----	2175

Db	56194	CCAGCCGAAGACTATATCCAGACTCCGATATGTTTCACTACATCGGTACCCCATTTAGGACC	56135
Qy	2176	-----	2175
Db	56134	ACCCACAGCACCCTAACAAAAGGGCATCAGCCTCTTGGAGGCTTCCAGGGCCTCATCTGG	56075
Qy	2176	-----	2175
Db	56074	AAGTGAACACCTGTAGCATCGACCTGCAGGGGGGGGGCGCTGAGGTCTGCCTCGTG	56015
Qy	2176	-----	2175
Db	56014	AAGAAGTGTGTGACTCATACAGCCCTGAATCGGCCCATCATCCAGCCAGAAAGTGA	55955
Qy	2176	-----	2175
Db	55954	GGGAGCCACGGTTGATGAGAGCTTGTGTAGTGGACCAGTTGGTGATTTGAACTTTT	55895
Qy	2176	-----	2175
Db	55894	GCTTTGCCACGAACGCTCTCGGTGTTCGGGAAGATGCGTGATCTGATCCTTCAACTCAG	55835
Qy	2176	-----	2175
Db	55834	CAAAAGTTCGATTTATTCACAAAGCGCGTCCCGTCAAGTCAGCGTAATGCTCTGCCA	55775
Qy	2176	-----	2175
Db	55774	GTGTTACACCAATTACCAATTCTGATTAGAAAACCTCATCGAGCATCAAAATGAACATG	55715
Qy	2176	-----	2175
Db	55714	CAATTATTTCATATCAGGATTATCAATACCATAATTTTGAAAAAGCGTTTCTGTATGA	55655
Qy	2176	-----	2175
Db	55654	AGGAGAAACTCACCGAGGAGTTCCATAGGATGGCAAGATCCTGTTATCGGTCTCGAT	55595
Qy	2176	-----	2175
Db	55594	TCCGACTCGTCCAACATCAATACAACCTATTAAATTTCCCTCGTCAAAATAGGTTATC	55535
Qy	2176	-----	2175
Db	55534	AAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGATGGCAAAAGCTTATGCAT	55475
Qy	2176	-----	2175
Db	55474	TTCTTTCCAGACTTGTTCTACAGGGCAGCCATTACGCTCGGCATCAAGATCACTCGATC	55415
Qy	2176	-----	2175
Db	55414	ACCCAAAGGTAATTCATTGCTGAATCGCGTTTGACGAGACCGAATTCGGGATCGTGGTAT	55355
Qy	2176	-----	2175
Db	55354	AAAGCCATTTCAACAGGATCGAATCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	55295
Qy	2176	-----AGA	2178
Db	55294	TAAGGGGTGGACTGAACAGGATGACACGGCATTGCAACCGGAAACCCAGGTTTCGGGCCAA	55235
Qy	2179	TACTCACAGCTGGCCACAGCTGGGCAAGGCTCTCGTGAGTGGAGTGGACTCGAGTCCCTGGA	2238
Db	55234	TACTCACAGG--TGCCACAACCTGGGCAGG--CTCTCGTGAAGTGACCCGA--TCCCGTGA	55181
Qy	2239	GCAGGAGTGTGGAGGAGCCATCCCTCTGTGATGCTGGCAGTAAAGGAGGACCTCGGAG	2298
Db	55180	GCAGGAGTGTGGAGAACGCCATCCCGTGTGATGCTGACGTGCGCATTAAGAGGACTTCGGAG	55121
Qy	2299	TGGACCCGAGCCAGGAATACGAATGACCAAGGCCAAGGGAGGAGGACAGAGGCCCC	2358

Db	55120	TGGACCCGAGCCAGGAATATCGAATGACCCCAAGGCCAAGGAAGGAGGACAGAGAGCCCC	55061
Qy	2359	CAGAGTGGTGGAGAGTGGAGTGCCTGGGACCTTGTGTGCAATAGAGAGTCTCCACA	2418
Db	55060	CAGGAGTGGTGGAGAGTGGAGTGCCTGGAGACCTTGTGTGCAATAGAGAGTCTCCACA	55001
Qy	2419	CCAGA-----	2423
Db	55000	CCAGATGCTTCCAGATTTCTGTGCTCTGTGCTTGTGTCAGCCAGGCTTGCAGTTTAT	54941
Qy	2424	-----	2423
Db	54940	TTTTCACAGTGACAGAGAGAGAGAGAGGCTGCATGTGTACCGTGTGTGGCAAGGC	54881
Qy	2424	-----	2423
Db	54880	AGGCGCTTGGCTGGGCGAGGGGGCCCCCTGCTTCTTTCCACAGCTTTCTTCCNACAGCA	54821
Qy	2424	-----	2423
Db	54820	GGCAGTGGGCTGCGGGCTGTGCGGTGCTCCCTGAGGAGCTTTATTGTTACTGTCACA	54761
Qy	2424	-----	2423
Db	54760	TAGTAGTATGTTCCAGGCCAGCCAGAGTGGCGTGGCAGGAGGCTGAGGCCCGGCCCT	54701
Qy	2424	-----	2423
Db	54700	CTGGGAAGGAGCTGTGGAGGAGAGACAGCCCATGCTGGGCACGGGCAGACTGGGTCCA	54641
Qy	2424	-----	2423
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Job time : 2935 secs

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Db 83095 GCTGCTTACGATCTCGGCGCTGGAGCCAGCTGTCCCTCTCTCTCAGGCTCCATCCGAAC 83154
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Qy 2424 ----- 2423
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Qy 2424 ----- 2423
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Db 83455 GAAACTGAGGCACAGGAGGTTTCCCAAGGTCACATACTGCTTAATAGCAGGGTAGAC 83514
Qy 2424 ----- 2423
Db 83515 AGGTGAAGTAACGTGGATGTATCAGCCATGCCCTTTCCCATGCCCCCGGCACTCCCCA 83574
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Qy 2424 ----- 2423
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Qy 2424 ----- 2423
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Qy 2424 ----- 2423
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Qy 2424 ----- 2423
Db 84055 AAAAGATGCCGAGGGATAAAGTCCAGAGCAGAGCAAGTCCAGGGCTGCAGCATCTCAGTG 84114
Qy 2424 ----- 2423
Db 84115 CTTACCCCAAGCATTAAGGCCAGAGCTGCTCCGTTGGAGCATAGGTTTCATGCCCCAG 84174
Qy 2424 ----- 2423
Db 84175 CTCCCCTGAGCCCTGCACAGCTCTGTCCCTGAGATGGGATGCTCTCCTCACTCATCACTG 84234
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	84415	GCCAGGCCATGGATCTATACATAAGTAAGTGTCCACCAGGCCCTGTCCAGTTGCTGCAGCC	84474
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	84895	TGGATGCTTCAGGCTTCACCCCTGACTCTGCTGCTTGTGCTTGGCCCTTGGAGAGCACT	84954
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Db	84955	TGGATCTTGGTTTCTCAGTGGAGTGAGTTGTAGGCAGCTAGAGCTGTGTTTGGACTGCTG	85014
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Db	85015	AATGGAGGGCTGTACTGGCTTTCCTGGCAGTTAGGGATCCTAGTAGCAGAGGGGTAG	85074
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Db	85075	AGACAGGGTCCCTTTTAGGGGGCCATGACAACAGGATATTTTAAGCTTACTTGACCACC	85134
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
Db	85975	AGAGACAAGGCTCAGGAGGCTGAGCCATGGAGTTGCTCTTAGCTTAGCCCCCATTCG	86034
QY	2424	-----	2423
Db	86035	AACCTTTTAGCTTCCCCAGAGCAAGCACTGTTCTTAAGGCTGCAGGCCACAGCCCCAGA	86094
QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423
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QY	2424	-----	2423

Qy	2424	-----	2423	-----	2423
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Db	87715	ATTGTGCTCTAGACCCCTCTTTAAGCCAGTGGAGTTTGAGGACATGCNANTAGTAATTTT	87774		
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Db	87775	ATAATCATTACTGGGCGAGTGTAAACAAACATTAGCACAGCTGGCAAGAGTGTAGGCAG	87834		
Qy	2424	-----	2423	-----	2423
Db	87835	ATGGTTCCTTTGGGATCCCTAAAAAAGCAGGATACAGCTGAGATCTCTGTGACACACTGTGA	87894		
Qy	2424	-----	2423	-----	2423
Db	87895	TTCAGAAACTGCTGGAACGTCTCCAGTCCCTGTGGTGTGCTGCCCTTGTAGGGGTGGTGCC	87954		
Qy	2424	-----	2423	-----	2423
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Db	88015	TATAGCTAAAAA	88032		

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RESULT 8
AC004241
LOCUS      AC004241      15517 bp      DNA      linear      HTG 14-MAR-1998
DEFINITION Homo sapiens, *** SEQUENCING IN PROGRESS ***, 14 unordered pieces.

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AC004241	155147 bp	DNA	linear	HTG 14-MAR-1998
LOCUS				
DEFINITION	Homo sapiens, *** SEQUENCING IN PROGRESS ***			14 unordered pieces.
ACCESSION	AC004241			
VERSION	AC004241	GI:2960506		
KEYWORDS	HTG: HTGS_PHASE1.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;			
	Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 155147)			
AUTHORS	Muzny,D., Aronson,A.D., Brundage,E., Carvelli,K., Chen,E., Di,W., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Ganesh,R., Garcia,C., Goodman,M., Gorrell,J.H., Haywood,M., Jackson,L., Kampal,R., Karpeth,S., Leal,B., Li,Y., Liu,W., Logan,O., Lu,J., Ly,T., Martinez,C., Oswal,G., Perez,L., Rashid,N.D., Rowland,K., Savage,L., Scherer,S., Shen,H., Timms,K.M., Todd,J., Vo., Worley,K.C., Yu,W., Chinault,C., Nelson,D. and Gibbs,R.A.			
TITLE	Direct Submission			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 155147)			
AUTHORS	Worley,K.C.			
TITLE	Direct Submission			
JOURNAL	Submitted (28-FEB-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
COMMENT	[WARNING] On Mar 21, 1998 this sequence was replaced by a newer version gi:2980958.			
	On Mar 14, 1998 this sequence version replaced gi:2943840.			
	* NOTE: This is a 'working draft' sequence. It currently			
	* consists of 14 contigs. The true order of the pieces			
	* is not known and their order in this sequence record is			
	* arbitrary. Gaps between the contigs are represented as			
	* runs of N, but the exact sizes of the gaps are unknown.			
	* This record will be updated with the finished sequence			

